APPENDIX A: DNA SEQUENCES

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>RXA00005
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>RXA00012-upstream
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>RXA00012
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>RXA00019-upstream
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>RXA00019

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>RXA00046
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>RXA00210
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>RXA00210-downstream
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>RXA00217-upstream
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>RXA00217
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>RXA00227
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>RXA00263
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>RXA00265-upstream
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>RXA00265
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>RXA00280-upstream
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>RXA00280
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>RXA00304
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>RXA00314
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>RXA00331-upstream
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>RXA00331
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>RXA00333-upstream
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>RXA00333
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>RXA00454
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>RXA00532
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RXA00568-upstream
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>RXA00568
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RXA00588-upstream
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>RXA00588
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>RXA00976-downstream
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>RXA00985-upstream
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>RXA00985
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>RXA00998-upstream
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>RXA00998
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>RXA00998-downstream
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>RXA01020-upstream
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>RXA01020
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>RXA01061
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>RXA01061-downstream
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>RXA01072-upstream
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>RXA01072
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>RXA01124
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>RXA01179-upstream
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>RXA01179
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>RXA01199-upstream
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>RXA01199
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>RXA01223-upstream
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>RXA01223
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>RXA01223-downstream
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>RXA01226-upstream
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>RXA01226
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>RXA01226-downstream
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>RXA01228-upstream
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>RXA01228
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>RXA01228-downstream
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>RXA01252-upstream
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>RXA01252
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>RXA01264-upstream
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>RXA01264
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>RXA01264-downstream
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>RXA01265-upstream
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>RXA01265
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>RXA01265-downstream
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>RXA01274-upstream
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>RXA01274
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>RXA01274-downstream
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>RXA01278-upstream
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>RXA01278
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>RXA01283
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>RXA01284
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>RXA01327-upstream
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>RXA01327
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>RXA01327-downstream
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>RXA01328-upstream
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>RXA01328
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>RXA01329-upstream
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>RXA01344-upstream
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>RXA01621
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>RXA01648-upstream
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>RXA01648
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>RXA01649-upstream
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>RXA01649
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>RXA01650-upstream
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>RXA01651-upstream
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>RXA01651
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>RXA01680-upstream
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>RXA01680
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>RXA01710
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>RXA01723-upstream
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>RXA01723
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>RXA01724-upstream
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>RXA01724
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>RXA01726
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>RXA01730
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>RXA01733
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>RXA01818
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>RXA01819-upstream
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>RXA01819
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>RXA01837
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>RXA01841
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>RXA01852-upstream
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RXA01863-upstream
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>RXA02110-upstream
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>RXA02110
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>RXA02130
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>RXA02130-downstream
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>RXA02167-upstream
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>RXA02167
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>RXA02174
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>RXA02182-upstream
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>RXA02182
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>RXA02204
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>RXA02228
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RXA02243-upstream
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>RXA02251-upstream
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>RXA02251
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>RXA02252-upstream
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>RXA02260-upstream
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>RXA02260-downstream
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>RXA02290-upstream
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>RXA02291-upstream
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>RXA02291
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>RXA02323
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>RXA02385-upstream
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>RXA02385
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>RXA02386
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>RXA02388
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>RXN02919
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>RXN02919-downstream
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>RXN02938-upstream
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>RXN02938
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>RXN02949-upstream
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>RXN02988
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>RXN02989-upstream
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>RXN03033
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>RXN03038-upstream
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>RXN03038
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>RXN03040-downstream
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>RXN03049-upstream
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>RXN03049
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>RXN03049-downstream
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>RXN03051-upstream
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>RXN03051
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>RXN03052
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>RXN03054-upstream
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>RXN03054
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>RXN03069
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>RXS00170 - upstream

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GCCACTGGTGGCGAAACCACCGTGAAGTACACCAGCGACCAGAACTCTGAGGTTACTTTCGTGCCGTTT
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TGGGCTCAGCAGGGCGCTGACCTTGGCCCTCTGGGACTTCCAACCAGTAATGAATACACCGTTGGCGAA
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CTGAAC

>RXS02641 – downstream
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>RXS02650 – upstream
GAATTTTTGCTGCAACTGTGTAAAAACCAGCGCTGAATTAAAGATCACCTTTCACCCTTAATTGAGCCT
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>RXS02650
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>RXS02650 – downstream
TGATGAACAACCGACAAAGCAGA

>RXS02760 – upstream
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>RXS02760
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GCTGCTGCAGAGTCCGAAGCTCCAGTAGAAGAGGACGAAGAGGCTGACAGCCTTGCTCAGGCGGCTGCT
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>RXS02760 - downstream
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>RXS02830
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>RXS02830 - downstream
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>RXS02990 - upstream
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>RXS02990
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>RXS02990 - downstream
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>RXS03098 - upstream
GACCGTTTTGTCGATCGCACCGCTGCTGGCTCGCACCATCAACGAGATCTTCGAAAACGGTTCCGTCAC
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>RXS03098
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ATT

>RXS03098 - downstream
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>RXS03175
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>RXS03175 - downstream
TAAAATGCTGCTGACAATTCTAT

>RXS03207 - upstream
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>RXS03207
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GTCATCCGTTTGCGCTACGGCCTCGATGACGGTGTGCCACGCACCCTTGATCAGATTGGTCGCCGCTTC
GGACTGTCCCGTGAGCGCGTCCGCCAGATAGAGCGTGAAGTCATGAGTAAGCTCCGCGATGGAGAGCGC
GCATCACGTCTTCGTGAGTACGCCCAG

>RXS03207 - downstream
TAAAAGCGTGAACTAACAATCGAAGCGTCG

Appendix B: AMINO ACID SEQUENCES

```
> RXA00005 (1-1608, translated) 536 residues
MHHEQPEGCE VGIRRTIPEE SRTAFLDMIN QGMSGLAAST AVGVSEFTGR KWAKAAGVKL
TRGPRGGNAF DTAEKLEIAA SMLEKGCLPR EIGEYVGMTR ANISLWRKQG PDKLRQRAAT
LRTGKRAAEF IHAPVMGPYY GPRTLHQVLR EDYTTLFDEL SALGLPAQVC GALLHLAPPP
SLRFSYMSCV VPLFADEIKV VGQGTRLSLE EKMMIQRFHD TGVSAAEIGR RLGRCRQTIS
RELRRGQDDD GRYRARDSYE GAIRKLARPK TPKLDANRRL RAVVVEALNN KLSPEQISGL
LATEHANDSS MQISHETIYQ ALYVQGKGAL RDELKVEKFL RTGRKGRKPQ SKLPSRGKPW
VEGALISQRP AEVADRAVPG HWEGDLVIGG ENQATALVTL VERTSRLTLI KRLGVNHEAS
TVTDALVEMM GDLPQALRRS LTWDQGVEMA EHARFSVVTK CPVFFCDPHS PWQRGSNENT
NGLVRDFFPK GTNFAKVSDE EVQRAQDLLN YRPRKMHGFK SATQVYEKIV VGASTD

> RXA00011 (1-357, translated) 119 residues
VNTTDSAVRL THIPTGIVVT CQNEKSQIQN KASAMRVLQA KLLERKRQEE RAEMDALGAG
GNASWGNQMR SYVLHPYQMV KDLRTNFEVN DPQKVLDGDI DGLLEAGIRW RMAESQSAE

> RXA00012 (1-876, translated) 292 residues
MRPEFSAELS ELDSTLTTIE KVLNPQEMSD RVRELEAQAA DPSLWDDPDH AQQVTSELSH
VQAELRKITD LRQRIEDLPI MVELAEEEDG DTSIAEEELA DLRSLIDALE VKTMLSGEYD
AREAVINIRS GAGGVDAADW AEMLRMYTR WAEKNGHKVD IYDISYAEEA GIKSATFVVH
GDYMYGQLSV EQGAHRLVRI SPFDNQGRRQ TSFAEVEVLP VVEKVDSIDI PDADVRVDVY
RSSGPGGQSS EHHRLCRAPD PHPNRHRGDL PKREITDPKQ GIRDACSPGK TA

> RXA00016 (1-894, translated) 298 residues
VIRFRFVDDA RKTYSVKRIC DVLKLNRSSY YKWKSTAFTR EKRLLSDAIL GVQVKTVFTT
HSGCYGAKRI AAELKDQIGH DLANHKRVAR IMRSLKLFGY TKKRKVTTTV PDKTKTVFPD
LVGRKFTADK PNQLYVGDIT YLPIQDGSNM YLATVIDCYS RRLVGFSIAD HMRTSLVQDA
LLMAKDQRGN LKGAIFHSDH GSVYTSHAFQ ETCKKLGIRQ SMGSIGTSAD NALAESFNAA
MKREVLQDSK TFENQLCCRR DVFRWCTRYN TVRRHSWCRY LAPVVFEERG PAILRSAS

> RXA00017 (1-294, translated) 98 residues
MPRKTYTEEF KRDAVALYEN SAGTSIQKIA NDLGINRMTL KNWITKYGAN STPHGANTAT
ALSEAERIRQ LEKENALLRE ERDILRKAAK YFAEETNW

> RXA00019 (1-1860, translated) 620 residues
MTVTSPAALA LSDMSYVDII KKKRGWTTEF FHSTINTGET TTPLPDSDRA TALIHDHITK
AQEITIITDF DMDGISAGVI AYAGLAELGA QVNMVVPDYR GERNVTASDI DRALELYPAT
SLIITCDVGI GSHEGIARAH ERSIAVLVTD HHMEVEPCQA DVVLNPNRID SDYPNKDICG
AQVIFATLSD YARRYRADKI IDINLLAVFS GIGALADVMP LTRDTRPTVK QAIALLRLAI
PQVSKNRFGG WDTYAARSVN PDTSTLMHIV NASQHDHRFI AAFQGISILL GELIAQKKLV
NIDNISESFI GFTLGPMFNA TRRVGGDMHD SFLVFAPHAA LASQPSMNPN RHAAISRIID
NNERRKELSK SSYAAVHSSD QPYAPFVWLS EAPSGILGLI ASQLTRESDV PAIVINPDTL
SGSARSPEWA PIITQVNTLS AQGHGGIHAA GHEYACGMRF DNHDDIVTFV ATLDALDKNT
PREAQPADLH LVDIDHARPV LDNPSLTQEL STVDAAVDAA QLLVLIDQLD QLQPFGHGFT
YPRIDVTFRP AETEFKVMGQ HHQHLKVITH SGLTLLWWNK AQQLDEIAQS ELVTMSVELD
VNMFRGFISP QGIVSACTVI

> RXA00046 (1-696, translated) 232 residues
MDLNTQRSKL YAQLQGQLIV SVQAPDGHAM RDTHTLTHVA AACVDGGAPA IRCGGYGGLE
DIRSISNRVD VPVFGLTKEG SEGVYITPTR DSVRAVAESG ATVVCADATF RPRPDGSTFA
ELVTVAHDSG ILIMADCATP EEVLSAHKAG ADFVSTTLAG YTEHREKTVG PDFDCLREAR
ELVPDAFLIG EGRFSNPADV AHGRLIGANA IIVGTGITDP GFITGQFASL LH

RXA00053 (1-393, translated) 131 residues
VKKRINVTGA VLVKENRILA AQRGPEMSLP GYWEFPGGKI EQGETPEASL ARELKEELLC
DATVGEHLTT TEHEYDFGIV VLSTYFCTLN DAEPQLTEHA EIRWVAPHEL ESLEWAPADI
PAVKLLVEQL A

> RXA00057 (1-99, translated) 33 residues
```

LGSIGTSADN ALAESFNAAL RREVLQDSKT FAN

RXA00069 (1-1383, translated) 461 residues
VAQQSIIDTV VNLCKRRGLV YPCGEIYGGT RSAWDYGPLG VELKENIKRQ WWRSMVTSRP
DVVGVDTSVI LPRQVWVTSG HVEVFTDPLV ESLNTHKRYR ADHLLEQYEE KHGHPPVNGL
ADINDPETGQ PGNWTEPKAF SGLLKTFLGP VDDEEGLHYL RPETAQGIFV NFKNVMNTSR
MKPPFGIANI GKSFRNEITP GNFIFRTREF EQMEMEFFVK PGEDEEWHQH WIDTRLQWYI
NLGIKPENLR LYEHPQEKLS HYSKRTVDIE YAFNFANTKW GELEGIANRT DYDLRVHSEG
SGEDLSFFDQ ETNERWIPFV IEPAAGLGRA MMMFLMDAYH EDEAPNSKGG VDKRVVLKLD
RRLAPVKVAV LPLSKKDTLT PLAEKLAAEL REFWNVDYDT SGAIGRRYRR QDEIGTPFCV
TVDFDSLEDN AVTVRERDTM EQVRVPLDEL QGYLAQRLIG C

RXA00102 (1-768, translated) 256 residues
MPEGDSVFQL SRKLQFMRGR EVLETSLRVP SVALHDFTGQ TVNRVWPYGK HLFMQFGEEI
LHTHLKMEGT WAVHRKGDRW RKPGHTARVV LVLSENIEVV GHSLGFVRVF PANRYSEEIA
YLGPDVLAEE FDINTARNNI ASNPSRTIGE ALLDQSNLAG VGNEYRAEIC FLMGVHPATQ
VGYVDVEKAL KITRRLMWEN RNSPIRVTTG VRRAGESTYV FGRNNKPCRR CRTPIVKAEL
GERIIWWCPR CQPLNS

> RXA00107 (1-237, translated) 79 residues
MSNVTIYATD WCPYCRSLLK GLDGQEYDLI DVDQDEEAGE WVKSVNDGNR IVPTVRYSDG
THATNPLAAE VIAKIEALA

> RXA00124 (1-732, translated) 244 residues
MTKDVHYEVD ERKKTVGVKE EGVEYVEDQL GIDNLYAPEH SQLVSYLNNA IKAQELFTRD
KDYIVRNGEV MIVDGFTGRV LAGRRYNEGM HQAIEAKERV EIKNENQTLA TVTLQNYFRL
YTKLAGMTGT AETEAAELNQ IYKLDVIAIP TNRPNQREDL TDLVYKTQEA KFAAVVDDIA
ERTEKGQPVL VGTVSVERSE YLSQLLTKRG IKHNVLNAKH HEQEAQIVAQ AGLPGAVTVA
TNMA

> RXA00125 (1-765, translated) 255 residues
VFGLSKVLRV GEGRAVKRLH KIADQVIALE DKFANLTDEE LKAKTAEFKE RIAGGEGLDE
IFLEAFATAR EAAWRVLGQK HYHVQIMGGA ALHFGNVAEM RTGEGKTLTC VLPAYLNALE
GKGVHVVTVN DYLAKRDAEM MGRVHRYLGL EVGVILSDMR PDERREAYAA DITYGTNNEL
GFDYLRDNMA RSLSDLVQRG HNYAIVDEVD SILIDEARTP LIISGTSRRH IAVLQRLRTD
RPTHDQGRSL RSRRT

> RXA00138 (1-561, translated) 187 residues
VATTADFKNG LVLKNEGKLQ QIIEFQHVKP GKGPAFVRTK LKDVVTGKTI DKTWNAGVKV
ETATVDRRDV TYLYNDGTSF IVMDDKTFEQ YELSPDAFGD AGRFLLENMR VQVSFHEGEA
LFGELPVSVD LRVEHTDPGL QGDRSTGGTK PATLETGAEI QVPLFIETGN VLKVDTRDGS
YLSRVNN

> RXA00172 (1-450, translated) 150 residues
MFGSSFKEQT TNPRSQRVSY LRVSSTDQNL ARQREAVNHS GHIDREFTDE LSGGAKSHRP
GLEDCINYLR EDDVLVVASI DRLARSLVDL RVIIDRITDK GASVIFLKEN LTFAAGRDDP
RANLMLGILG SFAEFERSII RERQAEGIAL

> RXA00184 (1-1173, translated) 391 residues
MSTVHDEMGV MNTTVKFLHS SDLQIGMTRW FLSDEAQARF DDDRIRAIEK MGKIARKNQC
EFIVLAGDVF EHNSLEQRTT GRALEALRSL KLPVYLLPGN HDPLTADSLF YRAKDIDGVT
ILSDTTVHGV APGVEIIGAP LLHKMATSDL VAEALKDLEP TSNVRIAVGH GQAEARTTDH
RADLIDLNTV EAKLADGTID YLALGDTHSA QPVGTSGKVW FSGAPETTDF HDLDPDRVGG
EVNSGKVLIV SASKGDVSVE EVEVGKWTFH ALSKEITSGT DVEDFLDTLQ AYPDKSRTVI
KYGLRGTITL EQNRRLEEGI AGLEDVFASL KPRERTTDLV LEPGEEELAN LDATGYAAEV
LRELADSVVN GAAPEEDRDA LNLLFRLSRE V

RXA00209 (1-1491, translated) 497 residues
MTNKYLVEGS ENELTTKTAA ELAGLIHSRE VTSREVTQAH LDRIAAVDGD IHAFLHVGQE
EALNAADDVD KRLDAGEAPA SALAGVPLAL KDVFTTTDAP TTAASKMLEG YMSPYDATVT
RKIREAGIPI LGKTNMDEFA MGSSTENSAY GPTHNPWDLE RTAGGSGGGS SAALAAGQAP

```
LAIGTDTGGS IRQPAALTNT VGVKPTYGTV SRYGLIACAS SLDQGGPTAR TVLDTALLHE
VIAGHDAFDA TSVNRPVAPV VQAAREGANG DLKGVKVGVV KQFDRDGYQP GVLEAFHASV
EQMRSQGAEI VEVDCPHFDD ALGAYYLILP CEVSSNLARF DGMRYGLRAG DDGTRSADEV
MAYTRAQGFG PEVKRRIILG TYALSVGYYD AYYLQAQRVR TLIAQDFAKA YEQVDILVSP
TTPTTAFKLG EKVTDPLEMY NFDLCTLPLN LAGLAGMSLP SGLASDTGLP VGLQLMAPAF
QDDRLYRVGA AFEAGRK
```

> RXA00210 (1-297, translated) 99 residues
```
VPEISRDQVA HLAKLSRLAL TEEELEQFAG QIDDIVGYVS AVQNVDAAGV EPMSHPHSIA
TTMREDVVHK TLDAAAALDQ APAVEDGRFM VPQILGEGD
```

RXA00217 (1-1095, translated) 365 residues
```
MRVLAAMSGG VDSAVAASRA VAAGHEVVGV HLALSQDPQT VRESSRGCCS LEDSADARRV
CDKLGIPFYV WDFSDRFKED VIDNFIDSYA IGETPNPCLR CNEKIKFAAL LERGIALGFD
AVVTGHYARL TQPADGGDGY LRRGVDPNKD QSYVLGVLGA HEIEHCMFPV GDTIKPEIRE
EASAAGFSVA KKPDSYDICF IPDGNTQAFL GKHIGMRPGM IVDQEGTHLR EHAGVHEFTI
GQRKGLDIKA PAADGRPRYV TDIDAKTGTV TVGTRENLKI STIHADRLKF LHPAMDGQID
CEVQVRAHGG VVSCSATIDR DADFMVLNLN EPLQGVARGQ AAVLYLPDAD GDIVLGSGTI
CHTES
```

> RXA00227 (1-798, translated) 266 residues
```
MVMQGIGGRK LAATVLLVRD GIINGRPDVE VYIQERVSTM ANFPRATVFP GGGVDSRDFA
DGHGKEVWRG PSAEEWGVRL GVEPHVAYAL VFAAVRELFE EAGTLLAEHT DGSGLVKNAG
QYHGYRELLE THEMSLTDML QSENLAIRSD LIVPFARWAS PEGNREQFDT FSFVAVEPEG
QCADGNTSEA SSTGYFPARL ILDGWRAGLL RLVIPTWASL FELSQFKTVE ELLEYSAQVD
MSPVLDDAVD NPRYAEFYQA MRTERF
```

RXA00263 (1-1308, translated) 436 residues
```
MKSTGNIIAD TICRTAELGL TITGASDAGD YTLIEADALD YTSTCPECSQ PGVFRHHTHR
MLIDLPIVGF PTKLFIRLPR YRCTNPTCKQ KYFQAELSCA DHGKKVTHRV TRWILQRLAI
DRMSVHATAK ALGLGWDLTC QLALDMCREL VYNDPHHLDG VYVIGVDEHK WSHNRAKHGD
GFVTVIVDMT GHRYDSRCPA RLLDVVPGRS ADALRSWLGS RGEQFRNQIR IVSMDGFQGY
ATASKELIPS ARRVMDPFHV VRLAGDKLTA CRQRLQREKY QRRGLSQDPL YKNRKTLLTT
HKWLSPRQQE SLEQLWAYDK DYGALKLAWL AYQAIIDCYQ MGNKREAKKK MRTIIDQLRV
LKGPNKELAQ LGRSLFKRLG DVLAYFDVGV SNGPVEAING RLEHLRGIAL GFRNLNHYIL
RCLIHSGQLV HKINAL
```

> RXA00265 (1-450, translated) 150 residues
```
MRSAHGPYID KFFPEPYKNM LELTKTLRKI YPDVDLPTSL IELVNVRVSQ INGCGTCLSL
HVPAARRAGV PEKKLDALAA WQMVDEFTVE EKAALQLAES LTLLESREGH LAARTACSVF
AEEQVAALEW AIIAINAFNR ISIASGHPLL
```

> RXA00280 (1-501, translated) 167 residues
```
VDTMKGDGDG WAAAPNGGAV WGKNGAAGLL LVADKQMLMQ HRAAWTNNGD TWALPGGARD
SHETAAESAL REAFEETGIL PDDVEVLDSI VTAGPFPADP ERPELAGNWT YTTVIARTKT
GETLDTTANE ESLELRWVDI AAVDSLALMP AFAKAWPSLR KLLNTTE
```

> RXA00304 (1-693, translated) 231 residues
```
MTAPSTQDLA TTEREVDPGS RRGQTNDNPS QDLVRVYLNG IGKTALLTAE DEVELAQTIE
VGLYAEHLLK NSEEPLTRAM KRDLKVLAKD GKKARSHLLE ANLRLVVSLA KRYTGRGMPL
LDLIQEGNLG LIRAMEKFDY SKGFKFSTYA TWWIRQAITR GMADQSRTIR LPVHLVEQVN
KLSRIKRELY QHLGREATNE ELAEESGIEE SKIEMLLRQS RDPVSLDMPV G
```

> RXA00314 (1-1380, translated) 460 residues
```
VTLRIFDTGT RTLRDFKPVQ PGHASVYLCG ATPQSSPHIG HVRSAVAFDI LRRWLMAKGL
DVAFVRNVTD IDDKILTKAS ENGRPWWEWV STYEREFTWT YNTLGVLPPS TEPRATGHVT
QMIKYMQRLI DNGFAYAVDG SVYFDVAAWS KAEGSDYGSL SGNRVEDMEQ GEPDNFGKRG
PQDFALWKAA KPGEPSWPTP WGDGRPGWHL ECSAMATYYL GEQFDIHCGG LDLQFPHHEN
EIAQAHAAGD KFANYWMHNH WVTMAGEKMS KSLGNVLAVP EMLKQVRPVE LRYYLGSAHY
RSVLEYSESA LSEAAVGYRR IESFLERVGD VEVGEWTPGF EVAMDEDIAV PKALAEIHNA
VREGNAALDK GDREAAEKLA SSVRAMTGVL GFDPVEWGSD AGADGKADKA LDVLISSELE
```

RRATARAEKN WAVADEVRDR LADAGIEVVD TADGATWKLQ

> RXA00331 (1-357, translated) 119 residues
MVGHMSNDHP YSPAKRVGNF IFVSGALSVD KDYQPVVGRK EAVDAALERM RERLATAGGE
LKDVVKLTYF VTDISLREEC NEQFREHFLE GRPARSFVGA SSLPYGATVE IDAIAMIED

> RXA00333 (1-534, translated) 178 residues
MAVPEFIVSL REKVGQDPLW LPAVTAVVIR DVPPGSPFHV VPDVLLVKRA DTGEWTPPTG
ICDPDEQPHV TAVREVKEET GLDVSVEALL GVGAVGPVTY QNGDVASYMD TTMRCVVSGD
SDEPHVGDDE NVDVAWFPIS KMPVTNQRFR MVIADAVAQL KHPQGYKPRM GYEKRNAR

> RXA00454 (1-864, translated) 288 residues
GDIATPAFIP VATKATVKTL TPEQIRETGA QAILSNAYHL YLQPGPDIVD EAGGVSAFEN
WHGPTYTDSG GFQVMSLGSG FKKVLAMDTT NLTRNDIKAA KKERMALVDE DGVDFKSVID
GSKHRFTPEV SMQIQHQLGA DIIFAFDELT TLVDTYDYQV ESVERTRRWA QRCLLEHERL
TQERVDKPLQ SLWGVVQGAQ FEDLRRQAVK GLLDLDRQAA DEGRRGFGGF GIGGALEKEN
LGTIVGWVCD ELPEDKPRHL LGISEPDDLF VAVEAGADTF YCVAPTRL

> RXA00458 (1-228, translated) 76 residues
MAGRYAPSPS GDLHFGNLRT ALLAWLFARS EGKKFLMRVE DIDEQRSFKE SAESQLADLS
ALGLDWDGDV LYQSTR

> RXA00495 (1-564, translated) 188 residues
LADTERELAD LVPQATAGDR RALQRIMEII HPIVLRYARA RIGGGRQPTA EDVAQEICLA
VATSIRNFVD QGRPFMAFVY GIASNKVADA HRAMSRDKST PIEEVPETSP DTFTPEDFAL
VSDGSNRVRE LLDLLSEKAR DILILRVIVG LSAEETAEMV GSTPGAVRVA QHRALTTLRS
TLEQQENK

> RXA00532 (1-585, translated) 195 residues
AIVKSKERND AHVTELALAA GRGDRAALTD FIRETQDDVW RLLAHLGGHE IADDLTQETY
LRVMSALPRF AARSSARTWL LSLARRVWVD NIRHDMARPR KSIVEYEDTG ATDASNAGIW
SEWIDVRTLI DALPPERREA LILTQVLGYT YEEAAKIADV RVGTIRSRVA RARADLIAAT
ATGDSSAEDG KSAQG

> RXA00539 (1-477, translated) 159 residues
MTSIHDISVT LNDGTETTMA DWAGHLLLIV NVASKCGLTP QYEGLQKLYE EYQDRGFFVI
GVPCNQFNGQ EPGTDAEVCA FAQNQYDVTF PLLSKTEVNG EGAHPLYKVL KEATDGSEIE
WNFEKFLVDA EGNTIKRFAP RTEPSAAEVV EAIEENLPI

> RXA00568 (1-1347, translated) 449 residues
VKSSVEKLSD TRSKITVEVP FSELKPEIDQ AYAALAQQVQ IPGFRKGKAP RQLIDARFGR
GAVLEQVVND MLPNRYAQAI EAEGIKAIGQ PNVEVTKIED NELVEFVAEV DVRPEFELPK
FEDITVEVPA IKADEEAIEA ELETLRARFS TLKDHNHKLK KGEFVTINIT ASIDGEKIEE
ATTEGLSYEI GSDDLIDGLD KALIGAKKDE TVEFTSELAN GEHKGKEAQI SVEITATKQR
ELPELDDEFA QLASEFDTIE ELRESTVSDV EAKQKNEQAA AIRDEVLAAA LGEADFALPQ
SIVDEQAHSQ LHQLLGELAH DDAALNSLLE AQGTTREEFD KKNVEDAEKA VRTQLFLDTL
SEVEEPEVSQ QELTDHILFT AQSYGMDPNQ FIGQLQQSGQ IANLFSDVRR GKALAQAICR
VNVKDSEGNE IDPKEYFGEE EVAETESEA

> RXA00588 (1-522, translated) 174 residues
MASVDKQYIT PETKAKLEEE LNALIAHRPA VAAEINERRE EGDLKENAGY DAAREMQDQE
EARIKQIYEL LANSTTEREG IIEGVANVGS VVHVYYDGDE NDKETFLIGT RAGASENPDL
ETYSEQSPLG AAILGAQEGD TRQYTAPNGS VISVTVVSAE PYNSAKAATL RGKN

> RXA00677 (1-216, translated) 72 residues
MAKEGAIEVE GRIVEPLPNA MFRVELDNGH KVLAHISGKM RQHYIRILPE DRVVVELSPY
DLTRGRIVYR YK

> RXA00687 (1-1320, translated) 440 residues
VSAIIQAFKD ADLRKKIFFT IAMIVLYRIG AQIPSPGVDY ATISGRLRDL TQDQSSVYSL
INLFSGGALL QLSIFAIGIM PYITASIIVQ LLTVVIPHFE ELKKEGQSGQ AKMMQYTRYL

```
TVALALLQSS  GIVALADREQ  LLGAGIRVLS  ADRNFFDLIV  LVITMTAGAV  LVMWMGELIT
EKGVGNGMSL  LIFAGIATRL  PTDGMNILGN  SGGVVFAVVL  ASVLILVIGV  VFVEQGQRRI
PVQYAKRMVG  RRQYGGSSTY  LPLKVNQAGV  IPVIFASSLI  YMPVLITQIV  NSGSLEVSDN
WWQRNIIAHL  QTPSSWQYIV  LYFALTIFFS  YFYVSVQYDP  AEQAENMKKY  GGFIPGIRPG
RPTAEYLGFV  MNRLLFVGSL  YLAVIAVLPN  IMLDLGVDAG  SAGATPFGGT  AILILVSVAL
TTVKQIESQL  LQSNYEGLLK
```

> RXA00736 (1-1887, translated) 629 residues
```
AGLVFPKVRK  HRDGAAMPLV  VITETDLTGN  RVGDIAGAKR  RPAKRRNKVD  PLALEPGDLV
VHETHGIGRF  VKMTERTISA  GDETSRREYI  VLEYAPSKRG  QPGDQLYVPM  DALDMLSRYV
GGEKPTLSKM  GGSDWKNAKK  KARAAVREIA  GELVELYAKR  QSAPGHPFAP  DTPWQKEMED
NFPYVETEDQ  MLAIDAVKED  MEKSVPMDRV  IIGDVGYGKT  EVAVRAAFKA  VQDGKQVAVL
VPTTLLAQQH  QSTFEERMTG  FPVTIKGLSR  FTSPAESREI  LSGLAAGSVD  IVIGTHRLLQ
TGVQWKNLGL  VIVDEEQRFG  VEHKEHIKAL  RTHVDVLTMS  ATPIPRTLEM  SMAGIREMTT
MLTPPEDRHP  ILTYVGPYED  KQVAASIRRE  LLRDGQVFFI  HNKVADIEKK  AREIRDLVPE
ARVVVAHGQM  SEELLEQTVQ  GFWDREYDVL  VCTTIVETGL  DISNANTLIV  ENAHHMGLSQ
LHQLRGRVGR  SRERGYAYFL  YPKGATLTEM  SYDRLATIAQ  NNDLGAGMAV  AMKDLEMRGA
GNVLGAEQSG  HIAGVGFDLY  VRLVGEAVEA  YRALADGKVV  DGTVKGPKEI  RVDLPVDAHI
PEKYINAERL  RLEIYRKLAQ  SESEVDLRL
```

> RXA00737 (1-480, translated) 160 residues
```
HPGNPTLVEM  LSRIADSQDV  DGMEALIPAL  TDTPMVPMLE  LMPENTHVLV  IAPEKVRRRI
ADLEATDAEF  LMAGWEAAAM  GADGPVAAEG  LDLEASSYRS  YESLEVSASK  SDVRWWTFAP
PGMFEASEEA  TLPLDFEAGP  APRGELPKID  AMMAQLLAHT
```

> RXA00753 (1-1422, translated) 474 residues
```
VVDGVGGYTE  QEVAEIHEAI  RQAQDSGAPN  DELIPGEMWS  DKVELPSTID  KAAADEAEIA
IAQQQSQPQA  RGLAAAAACQ  TFWPSPYQVC  GAILERYIQQ  GAQFGWMLLL  TEGQALNPDG
QGYRQRFMNG  FIYWHPSTGA  HAVNNYSAQV  WERNGWESGW  MGYPTGGEVP  VSGSNPIDGE
LSGWVQTFQG  GRVYRSPVLD  GFQVASINGL  ILDKWLELGG  PDSDLGFPIA  DEAVTADGVG
RFSVFQNGVV  YWHPQHGAHP  ILGNIYSIWR  EEGAESGEFG  YPIGDPEKYT  ENMANQVFEK
GELAANLYPN  PLEAFIEFLP  FANLEEAIEY  FENGLSNSRV  EANSLNAKKD  SIQCQSQSAN
IHVRTKSDGV  GIRVPKIGFK  ARMDCDLPGT  VSDVVGYGWI  YYDYWGRWAQ  AAYAQQFFGN
RNSVVQTNLE  AGCSGEKNTL  FWGTSYFQVT  YEGQPYFGQS  ATNYAYLPCT  IDRS
```

> RXA00755 (1-1275, translated) 425 residues
```
VPGKLRVHEL  AKQLGITSKE  LLATLKDKGE  FVKTASSTIE  PPVVKRMQEH  YGSSGSDKSD
TAAKPAAAKP  AAPKPAASAA  PKPGAPAKPA  APAAKPAPAA  PSAASAAKPG  AAPKPGVQAK
PAAAAKPGAP  AKPAAPAAPS  AAKSGSASKP  AAAAKPAFSG  PTPGDASKKA  EPAAKPGAEA
PRPGGMPRPM  GKPAPKPGAR  APRVANNPFS  TGGGERPAPR  PGGGPRPGGG  PRPGGGPRPQ
GQGRPGGQRD  GQRDGQRDGQ  GNRGGQRQGA  GAGGPRPQGG  PRPQGGSRPQ  GGSAQGAQGA
PSQERQGGGR  RPSPAMMPPT  PGQMPAKAPG  KGGRGGQAGG  GAGGGFNRGG  GTGGGAGRGG
RRGGTAGAFG  RPGGAPRRGR  KSKRQKRNEY  ESMQAPNVIG  GVRLPDGKGA  TIRLARGASL
ADFAD
```

> RXA00758 (1-1602, translated) 534 residues
```
MTLKKSLAVT  TAAALALSLA  ACSSDSSSDS  SSSSSGSEGG  DNYVLVNGTE  PQNPLVPGNT
NEVGGGRIVD  SIFSGLVYYD  VDGSPVNDVA  ESIELEGDKT  YRITIKDGQT  FTDGTPVTAE
SFVNAWNYNV  ANSTLSSYFF  ESILGYEEGV  ESMEGLQVVD  DTTFTVELTQ  PESDFPLRLG
YSAFFPLPES  AFDDMDAFGE  NPIGNGPYKL  QEWNHNQDAT  IVPNADYTGG  RQAQNDGVKF
IFYPTFDSAY  ADLLSDNLDV  LDAIPDSAFS  SFEDELSGRS  INQPSAVFQS  FTIPESLEHF
SGEEGVLRRQ  AISLAVNRDE  ITQTIFEGTR  TPATDFTSPV  IDGHSDSLQG  ADVLTYDPER
AQELWAQADE  ISPWSGEFSI  SYNADGGHQA  WVDATANSIR  NTLGIDAIGN  PYPDFKSLRD
DVTNRTINGA  FRTGWQADYP  SLGNFLGPLY  GTGAGSNDGD  YSNPDFDAKL  AEAANAADVD
ASTPLYNEAQ  EILLQDLPAI  PTWYSNAVGG  YSTNVDNVEF  QWNSQPAYYQ  ITKN
```

> RXA00824 (1-558, translated) 186 residues
```
MTSSAKWSIV  GVVAILAVIV  ALIPQLVGGE  SAEEAQGETS  TSKITTRPDC  VASGAAGVDL
PCLGGANGVG  NELATVVNLW  AWWCEPCRAE  LPIFDEFATT  HPELNVIGVH  ADQNAANGAA
LLEDLGVNLA  SYQDDSNLFA  GTLGLPGVVP  ITIVVSPDGN  VVDTFPQPFE  TIDDLETAVA
GALQNA
```

> RXA00896 (1-639, translated) 213 residues
MTVRPIVIHG DPVLHNPTQL VTEDVSELQE LIADMYETMD VANGVGLAAN QIGVSKRIFV
YDCPDDEGVM HKGCFINPVL ETSEIPETMP ADDGSDEEGC LSVPGEGFPT GRAHWAKVTG
LNEKGEEVSV EAEGFLARCF QHEVGHLDGF LYTDVLIGRW KRMAKKAIKA NGWTEPGLTW
MPGEDEDPFG HDAYVFPVSA ARNLPSAIVL LHV

> RXA00927 (1-1089, translated) 363 residues
MSDVERTEFE IPGGIPPRRN GGQGRAADTN VDANLKPDEY DAEVTLRPKS LTEFIGQPKV
RDQLSLVLTG AKNRGVVPDH VLLSGPPGLG KTTMAMIIAQ ELGTSLRMTS GPALERAGDL
AAMLSNLMEG DVLFIDEIHR IARPAEEMLY MAMEDFRIDV IVGKGPGATS IPLEIPPFTL
VGATTRSGML TGPLRDRFGF TAQMEFYDVP DLTKVVKRTA KILDVGIDND AAVEIASRSR
GTPRIANRLL RRVRDFAEVH ADGHITMGAA NAALIVFDVD EVGLDRLDRA VLDALIRGHG
GGPVGVNTLA VAVGEEPGTV EEVCEPYLVR AGMIARTGRG RVATAAAWRH LGLEPPEGTI
GDY

> RXA00928 (1-618, translated) 206 residues
MIASLRGTVI NIGLSSAVIE CNGVGYEVVT TPNTLSQLVR GEEALVLTTM VVREDAMKLY
GFIDNESREM FSVLQTVSGL GPRLALACES VLSPLEISQA ITNADAKTLQ RVPGVGKRMA
DRLIVELKGK VAAFAAGVVD EGGEQISLPN ANIASEVVVE QVSQALVGLG FSEKQSDDAV
SFVLAADPSL DTSGALRAAL AKLSGK

> RXA00929 (1-663, translated) 221 residues
MNHEGLRVMG IDPGLTRCGL SVVQAGRGRT VYPVSVGVVR TPPDAELAER LLRLSKAVGE
WMDEYTPDVI AIERVFERGN VSTVMNTAHA VGVLILAAAE RGLPVHMYTP SEVKKAISGN
GRADKKQMTV MITRILGLGE PPKPADAADA LSLAVCHCWR APMLMRAQSQ YSEQELEKRR
RVQQGKLGKA KSTYNAEQAQ SHASDPAKAA HPSQFQRTDT N

> RXA00935 (1-651, translated) 217 residues
SAASAWERWP KRAIALFVLI VVGVYALVLL TGDRSATPKL GIDLQGGTRV TLVPQGQDPT
QDQLNQARTI LENRVNGMGV SGASVVADGN TLVITVPGEN TAQAQSLGQT SQLLFRPVGQ
AGMPDMTTLM PELEEMANRW VEYGVITEEQ ANASLEEMNT AVASTTAVEG EEATEPEPVT
VSATPMDEPA NSIEATQRRQ EITDMLRTDR QSTDPTV

> RXA00937 (1-123, translated) 41 residues
VYREAGTMPA PALDDLVNQV KALDMDDVRR QVAEQQGSAE A

> RXA00938 (1-258, translated) 86 residues
MRPISGSAAG GATSDLAITA GGQTLDFYLS PKRNVAAAKR FLAKALRSNA SAGYPRVINT
DKAPSLARAI TELKSEGICP PTVEHR

> RXA00966 (1-528, translated) 176 residues
MTNPSEGTTP LAFRYTPELA NKIEGEWQNY WTDNGTFNAP NPVGDLAPAD GKALPEDKLF
VQDMFPYPSG AGLHVGHPLG YIATDVFARY NRMLGKNVLH TLGYDAFGLP AEQYAIQTGT
HPRTTTMANI ENMKRQLGAL GLGHDSRRAV ATTDPEFYKW TQWIFLQIFN SWFDAE

> RXA00968 (1-1002, translated) 334 residues
LIDDLELLDW TEKVKSMQRN WIGRSRGAEV DFSAEGETVT VFTTRPDTLF GATYMVLAPE
HELVDVLLEK AGSYEGVDAR WTNGQASPAE AVAAYRASIA AKSDLERQEN KEKTGVFLGV
YATNPVNGDQ ITVFIADYVL TGYGTGAIMA VPAHDERDYE FATVLGLPIK EVVAGGNIEE
AAFTESGEAV NSANDNGLDI NGLAKDEAIA KTIEWLEEKE LGRGTIQYKL RDWLFARQRY
WGEPFPIVYD ENGQAHALPD SMLPVELPEV EDYKPVSFDP EDADSEPSPP LAKAREWVEV
ELDLGDGKKK YTRDTNVMPQ WAGSSWYQLR YVDP

> RXA00975 (1-777, translated) 259 residues
LALEPAATQE LFRAEGVEMM FEHIKSSLHE FGTDFDVYYH ENSLFESGAV DKAVQVLKDN
GNLYENEGAW WLRSTEFGDD KDRVVIKSDG DAAYIAGDIA YVADKFSRGH NLNIYMLGAD
HHGYIARLKA AAAALGYKPE GVEVLIGQMV NLLRDGKAVR MSKRAGTVVT LDDLVEAIGI
DAARYSLIRS SVDSSLDIDL GLWESQSSDN PVYYVQYGHA RLCSIARKAE TLGVTEEGAD
LSLLTHDREG DLIRTLGEF

> RXA00976 (1-600, translated) 200 residues
MTPADLATLI KETAVEVLTS RELDTSVLPE QVVVERPRNP EHGDYATNIA LQVAKKVGQN
PRDLATWLAE ALAADDAIDS AEIAGPGFLN IRLAAAAQGE IVAKILAQGE TFGNSDHLSH
LDVNLEFVSA NPTGPIHLGG TRWAAVGDSL GRVLEASGAK VTREYYFNDH GRQIDRFALS
SSCSGEGRAN ARRRLWRRIH

> RXA00985 (1-495, translated) 165 residues
VLGHVLDALL RLLHPAMPFV TEVLWQALTD RTSIVVASWP TAADTNGGVA VDADAARRIG
DVEKLVTEVR RFRADQGVKP SQKVPARLDF VACDLQDLED SVRSLVRIEQ PEDDFAASAS
LEIRLSQATI TVELDTSGTV DVAAERKRLE KDLANAQKEL ETTAK

> RXA00998 (1-462, translated) 154 residues
MTSRDDQPQD LLSLAELAAT RALTTDELEA LNNANYGLDR NLGLRYTTIE PGRVVSELHV
ASKHLQVVGL VNGGVYAAIA ESTGSVASMI SAPGKMVVGI NNNTDFISAV SSGVIVAEAT
PIQLGGRTHL WQIECTHRGE VVARTTLRTM VLNK

> RXA01020 (1-747, translated) 249 residues
MTNTLWNSVD ELPIHDSWKP VLKPVEDAIR KLGVFLAEEE FLPPVDDVFR AFSYPFDAVK
VLIMGQDPYP TPGHAMGLSF STQPDVRPLP RSLNNIFKEL VSDVGSLGDS ASEQGALDLG
INAPGSVAGT QVALPADGDL RAWSNQGVAL FNRVLTVHPG QAGSHKGKGW EAVTEQAIKA
LAERDQPLVA ILWGKQAQEV QKFLGDTPCI CSVHPSPLSA SRGFFGSKPF SRANEILSSL
GATEIDWSL

> RXA01061 (1-408, translated) 136 residues
LRVNTVVAKL IEYVNYLTKT YPDTIPAGAV LPLIVMVSPI APHIAEELWK KLGHDDTVTY
EPFPTFEEKW LTDDEIELPV QVNGKVRGRI TVAADASQEQ VIEAALADEK VQEQISGKNL
IKQIVVPGRM VNLVVK

> RXA01072 (1-231, translated) 77 residues
MAITVYTKPA CVQCNATKKA LDRAGLEYDL VDISLDEEAR EYVLALGYLQ APVVVADGSH
WSGFRPERIR EMATAAA

> RXA01124 (1-1509, translated) 503 residues
RWVRAINMAC MTDVRVRFCP SPTGTPHVGL VRTALFNWAY ARHTGGKLVF RIEDTDAARD
SEESYSAIID SLRWLGMDWD EGVEKGGPHE PYRQSQRKDI YQDVLKQLID AGEVYPAYST
AEEVEERHKA AGRDPKLGYD NFDRDLTEEQ VAAFEAEGRK PVWRLRMPEQ DWKWTDLVRG
EVEFKSFTQP DFVVARSNGE PLYTLVNPVD DALMEVTHVL RGEDLLPSTP RQLALYEALK
RIGVAKATPA FGHLPFVMGE GNKKLSKRDP QSSLFNHRDN GIIPEGMLNY LALLGWSLSA
DQDIFGVDEL IANFDVADVL GNPARFDQKK LEAINADHIR LLEPKDFEAR LRAYMTEYTE
FPADYPAEKF AIAAAELVQTR IKVLSEAWDL LKFLVTADED LVFNEKAAKK NLKETAVEPL
NAGIAALEAV EEWTTPNIEA ALNKALIEDL GLKPRVAFGA LRIGISGEAV SPPLFESMEL
LGKESTLVRL KVTREQTPFV VAE

> RXA01179 (1-513, translated) 171 residues
MHSKEELTVR KGISRVLSVA VASSIGFGTV LTGTGIAAAQ DSAFDYGMDP NMNYNPIDDI
KDRPEGLSNL PYFGSKLTSW GSSYATASSG VVTSALPQYT DPRYPLGKDD LPKATIDMEP
EVLARLERFV GVDGDRIRQI NAYSPSMGRT IPLVWVVPKD NTVPCPTVYA L

> RXA01199 (1-771, translated) 257 residues
VTSPHNFVSG AIDLGEVKAR ADARQKAHEQ GPVTQGIASS LDVTMENLEN EVLRRSTQVP
VIVLVGTPRS PDSEQLKSDL TTLAAESGRK FIFGYVNADT DADVAQVFGV QGLPSVIAVA
AGRPLADFQG GQPADALKQW TDQVVQAVGG QLEGLPEEAT DGEQEDAPVE DPRFDAATDA
LNRGAFDEAI AVYESILAQE PNNADAKQAP RYRKAVGPAC HRWILRWMLS LLQMLIQQTL
IWPTQATDAA VVAGDPE

> RXA01223 (1-612, translated) 204 residues
MTSVSFLSKI QALFAPKPEL PAAKWLVVGL GNPGAKYEST RHNVGYMCQD MLIDAHQQQP
LTPATGYKAL TTQLAPGVLA VRSTTFMNHS GQGVAPIAAA LGIPAERIIV IHDELDLPAG
KVRLKKGGNE NGHNGLKSLT EELGTRDYLR VRIGISRPPA GMAVPDYVLE PVDHDQPGIE
LAAEAVDLLL AQGLSAAQNA IHSR

> RXA01226 (1-444, translated) 148 residues
AEELVSRSFG SFSVHKRSNT DIAQLPGLIV AKPRSFMNLS GTPIRALCDF FKISPANVIV
VHDELELDFG SVKLRQGGGD HGHNGLKSTS KSLGTKDYWK LSMGIGRPPG RMDPASFVLK
PFGKQELADI PIMAADAADL VEKHLQQG

> RXA01228 (1-216, translated) 72 residues
VHFIKENLIF SAESNALRAQ LMLSILGSFA EFERSIIRER QAEGIAWRKR PASTRAANAP
SPRTTSRKPG NG

> RXA01252 (1-654, translated) 218 residues
VFEGPLQDLI DELSRLPGVG PKSAQRIAFH LLNVDPSDIT RLQEALGGVR DGVQFCRICC
NISREEVCRI CSDSGRDGGT ICVVEEPKDI QVIERTGEFS GRYHVLGGAL DPLANIGPRE
LNISTLLQRI GGVLPDRELA DSTPENKLFD ATPTVREVIL ATDPNTEGEA TASYLGRLLK
DFPDLVISRL ASGMPLGGDL EFVDELTLSR ALSGRLQI

> RXA01264 (1-216, translated) 72 residues
MDELAQLGHT LWRRRKNVLA SFNIGASNGP VEAINGRLEH LRGITLGFRN LNHYILRCLI
QAGQLQRKIN VL

> RXA01265 (1-150, translated) 50 residues
MSVSATAKAL KIGWELVNQV ALDACRQLIY NDPRHLEVDE HVWKYTRKPG

> RXA01274 (1-1095, translated) 365 residues
MKLLRRIAAP AIALGIAMST IVTPSTAGAA EVTPADVAGD TALSTISDSA PADEASAPRW
RAHVNAADER VKEMWAYSPS MDRNVPLVVI TADESAGPRP VIYLLNGGDG GEGAANWVMQ
TDVLDFYLEK NVNVVIPMEG KFSYYTDWVE ENASLGGKQM WETFLVKELP GPLEEKLNTD
GQRAIAGMSM SATTSLLFPQ HFPGFYDAAA SFSGCAATSS LLPWEYLKLT LDRGNATPEQ
MWGPRGGEYN IYNDALINSD KLRGTELYVS NASGLAGEWE SVDSPRFEGL NQQVQSIAMA
ETVVTGGIIE AATNKCTHDL KAKLDSAGIP ADWNLRPTGT HSWGWWQDDL RGSWTTFARA
FELEA

> RXA01278 (1-2127, translated) 709 residues
VAQEVLKDLN KVRNIGIMAH IDAGKTTTTE RILFYTGINR KVGETHDGGA TTDWMEQEKE
RGITITSAAV TCFWDNNQVN IIDTPGHVDF TVEVERSLRV LDGAVAVFDG KEGVEPQSEQ
VWRQATKYDV PRICFVNKMD KLGADFYFTV GTIEDRLGAK PLVMQLPIGA EDNFDGVIDL
LEMKALTWRG VTPIGTEATV EEIPAELADR AAEYREKLLE TVAESDEELM EKYFGGEELS
IAEIKAAIRK MVVNSEIYPV YCGTAYKNKG IQPLLDAVVD FLPSPLDLGE TKGTDVKDPE
KVLTRKPSDE EPLSALAFKI AAHPFFGKLT FVRLYSGKVE PGEQVLNSTK NKKERIGKLF
QMHANKENPV EVAHAGNIYA FIGLKDTTTG DTLCDANAPI ILESMDFPDP VIQVAIEPKT
KSDQEKLGVA IQKLAEEDPT FTVHLDDESG QTVIGGMGEL HLDVLVDRMK REFKVEANIG
DPQVAYRETI RKPVESLSYT HKKQTGGSGQ FAKVIITIEP YAPEADELEE GESAIYKFEN
AVTGGRVPRE YIPSVDAGIQ DAMQYGFLAG YPLVNVKATL EDGAYHDVDS SEMAFKLAGS
QAFKEAVAKA KPVLLEPIMS VEITTPEEYM GEVIGDVNSR RGQIASMDDR AGAKLVKAKV
PLSQMFGYVG DLRSKTQGRA NYSMVFDSYA EVPANVAADV IAERNGTAS

> RXA01283 (1-1293, translated) 431 residues
TRQGVRVPVA AEVLDATGAV TGYTRHDLIE TSVSGRVLAG DATNAAGEVV LAAGTDLTEL
NIDLLVEAGI KDVKVRSVLT CQTPTGVCAK CYGKSMASGQ QVDIGEAVGI VAAQSIGEPG
TQLTMRTFHQ GGVGGDITGG LPRVQELFEA RVPKNCAPIA SVEGVIHLED EGNFYTLTIV
PDDGSDNVVY EKLSKRQGLA STRVAMESNA GAFIERTLTE GDRVTVGQRL LRGAADPHDV
LEILGRRGVE QHLIYEVQAV YRAQGVAIHD KHIEIIIRQM LRRGTVIESG STEFLPGSLV
DLSEAKLANS EAIGAGGQPA ELRSEIMGIT KASLATESWL SAASFQETTR VLTDAAINKR
SDKLIGLKEN VIIGKLIPAG TGISRYRNIS IKPTEAARNA AYSIPTYGES IYGDDGFGEF
TGASVPLDEA F

> RXA01284 (1-507, translated) 169 residues
VDHGKTTTTA AITKVLADTY PELNQAFAFD SIDKAPEEKE RGITINISHV EYQTEKRHYA
HVDAPGHADY IKNMITGAAQ MDGAILVVAA TDGPMPQTRE HVLLARQVGV PYILVALNKC
DMVEDEEIIE LVEMEVRELL AEQDYDEEAP IVHISALKAL EGDEKWGKQ

> RXA01327 (1-144, translated) 48 residues

MSIAATAKAL GLGWDLTCQL ALDMCHELIY YDPTHLEIVH VIGVDEHK

> RXA01328 (1-375, translated) 125 residues
LLDVVEGRSA DALRAWLARR SPAFRHQVRI VTMDGFQGYA TTSKQLLPAA RRVMDPFHVV
LLAGDKLTRC RQRLQQEKYH RRGLHDDPLY KNRKTLLTTQ KWLSKKKQSV LMSCLALIKT
TRHCN

> RXA01329 (1-291, translated) 97 residues
MADKRRAKTM MREIVDQMRL LKGQANRELA QLGRSLHKRL GDILAYFDVG ISNGPVEAIN
GRLEHLRGIA LGFRNLNHYI LHCLIHSGQL THKINAL

> RXA01344 (1-2547, translated) 849 residues
VLEGPILAVS RQTKSVVDIP GAPQRYSFAK VSAPIEVPGL LDLQLDSYSW LIGTPEWRAR
QKEEFGEGAR VTSGLENILE ELSPIQDYSG NMSLSLSEPR FEDVKNTIDE AKEKDINYAA
PLYVTAEFVN NTTGEIKSQT VFIGDFPMMT DKGTFIINGT ERVVVSQLVR SPGVYFDQTI
DKSTERPLHA VKVIPSRGAW LEFDVDKRDS VGVRIDRKRR QPVTVLLKAL GWTTEQITER
FGFSEIMMST LESDGVANTD EALLEIYRKQ RPGEQPTRDL AQSLLDNSFF RAKRYDLARV
GRYKINRKLG LGGDHDGLMT LTEEDIATTI EYLVRLHAGE RVMTSPNGEE IPVETDDIDH
FGNRRLRTVG ELIQNQVRVG LSRMERVVRE RMTTQDAESI TPTSLINVRP VSAAIREFFG
TSQLSQFMDQ NNSLSGLTHK RRLSALGPGG LSRERAGIEV RDVHPSHYGR MCPIETPEGP
NIGLIGSLAS YARVNPFGFI ETPYRRIIDG KLTDQIDYLT ADEEDRFVVA QANTHYDEEG
NITDETVTVR LKDGDIAMVG RNAVDYMDVS PRQMVSVGTA MIPFLEHDDA NRALMGANMQ
KQAVPLIRAE APFVGTGMEQ RAAYDAGDLV ITPVAGVVEN VSADFITIMA DDGKRETYLL
RKFQRTNQGT SYNQKPLVNL GERVEAGQVI ADGPGTFNGE MSLGRNLLVA FMPWEGHNYE
DAIILNQNIV EQDILTSIHI EEHEIDARDT KLGAEEITRD IPNVSEEVLK DLDDRGIVRI
GADVRDGDIL VGKVTPKGET ELTPEERLLR AIFGEKAREV RDTSMKVPHG ETGKVIGVRH
FSREDDDDL

> RXA01346 (1-1575, translated) 525 residues
MRTATKVIAT VMASTLAIGL ASCSSSSGTP DVNYVSVNGT EPQRGLIPGD TNENGGGRVV
DMLYSGLVYF DEAGVAQNDL AASIDQETDT TYKITLRDGI KFSDGSDITA TDFVDTWNFV
VENGLLNTSF FSPIKGYEEG VETLEGLNVV DDRTFTIELA QPDSEFTQRI GYYGFAPMPA
SARDDIDAFG ENPVSSGPYK LEQWDHNAEL KVVANEHYDG PRAANNDGLK YVFYAQNDAA
YSDLLAGNLD VLDLIPPSAY TTYEEELSGR SINQPAASYL ELSIRMESPN FEGQQGQLRR
QAISMAINRE EIAEQIFAGT YTPALDFTAP VLDGWRDDLN GNDVLTFQPD KARELWEDAE
EIAPFEGELQ ISYNADVPNR EWVDAVANSI SNELDVNATG NPFPDFKSFR DTYRTTGLDG
AYRTAWFADY PSIGNFLGPN YTSGVASNDA KYENPEFDQL IADAAAASTK EETFQAYAQA
QEMLLRDLPA IPLWYPNVVG GYSESVDNVS VNWKAIPVYW AITKQ

> RXA01347 (1-2049, translated) 683 residues
MVCVTDQNNE TTSQNRADKL PKSWDPKAVE ADLYQGWVDA GYFTADPASD KPGFSIVLPP
PNVTGQLHMG HALDHTLMDA LARRKRMQGF EVLWLPGMDH AGIATQTKVE EMLKETEGKT
RYDYDREEFI AKVWEWKQEY GGKIGEQMRA IGDSVDWSRE RFTLDDGLSR AVQTIFKKLF
DAGLIYQANR LVNWSPVLET AVSDIEVIYK DVEGELVSIR YGSLNDDEPH VIVATTRVET
MLGDVAVAVH PDDERYKDLV GQTLPHPFRD DLSLKVVADD YVDPEFGSGA VKITPAHDPN
DYALGLRHNL DMPTIMDKTG RIADTGTQFD GLTREEARIK VREELAAQGR IVKEIRPYVH
SVGHSERSGE AIEPRLSLQW FVKVEELAKM SGDAVREGDT TIHPKSLEPR YFDWVDNMHD
WTISRQLWWG HRIPIWYGPN DEIICVGPDE QAPEGYVQDP DVLDTWFSSA LWPFSTMGWP
EKTPELEKFY PTSVLVTAYD ILFFWVARMM MFGTFAAKET PELLGEGKDG RPQVPFTDLF
LHGLVRDEHG RKMSKSLGNG IDPMDWVENY GADALRFTLA RGANPGVDLP VGEDSAQSSR
NFATKLFNAT KFALMNGAVS EGLPAREELT DADRWIVDLL EQVRLDVDAY LDNYQFAKAN
EELYHFAWNE FCDWYLEIAK VQI

> RXA01355 (1-786, translated) 262 residues
VTDFSSASNA DDSTQDGRPG RRAGKSKKES KPTPWYIEIP VVVVLTLALI FVLQTFVGRM
YMIPSGSMEP TLHGCEGCTG DRILVEKVSY YFTDPEPGDV VVFKGTDSWN VGFTTQRSDN
SVIRGLQNLG SYVGLVAPDE NDLVKRIIAT GGQTVSCQAG DPGIMVDGKE VDDSYTLQPA
QFPIDETSGS TECGGNYFGP ITVPGGNYFM MGDNRTNSMD SRYHLGDQYQ GTIPEENIKG
KVQAIILPFS RIGGVDDPAI KG

> RXA01387 (1-369, translated) 123 residues

```
VLDVNVFDEL RIGLATADDI RRWSKGEVKK PETINYRTLK PEKDGLFCER IFGPTRDWEC
ACGKYKRVRY KGIICERCGV EVTKSKVRRE RMGHIELAAP VTHIWYFKGV PSRLGYLLDL
APK
```

> RXA01388 (1-132, translated) 44 residues
```
MNEEVLSANG TPMKLAGDDD DFDQAGASIG INLSRDERSD ADTA
```

> RXA01398 (1-636, translated) 212 residues
```
KETAEDYRYF NDPDLPPVIA PREWVEEIRA TLPELPWVRR ARIQEEWKLS DAEMRDLINA
NALDLIIETV EAGTTPDEAR AWWVSYISQK ANESGVELDA LGVAPAHVAR VVALVSEGKL
TNKLARQAID GVIAGEGDVD AVVAARGLEV VRDDGAIEKA VDDALAANPD IVEKYRAGNT
KVTGAIVGAV MKATRGKADP AQVNQLIAKK LA
```

> RXA01431 (1-321, translated) 107 residues
```
MSNVVAVTEQ TFKSTVIDSD KPVIVDFWAE WCGPCKKLSP IIEEIAGEYG DKAVVASVDV
DAERTLGAMF QIMSIPSVLI FKNGAKVEEF VGLRPKNEIV EKLEKHL
```

> RXA01432 (1-951, translated) 317 residues
```
MSEEQSAVAP KIHDVAIIGS GPAGYTAAVY AARADLNPIM FEGYEYGGSL MTTTDVENFP
GFEKGILGPE LMENMRAQAE RFGTDMHMEL VDRVDLTGDI KKLWVGDDEY HARAVILSMG
SAPRYLGVKG EQELLGRGVS ACATCDGFFF RDQDIAVIGG GDSAMEEATF LTKFARSVTI
VHRREEFRAS AIMLERAQKN EKIRFVTNKT VEEVIEADGK VSGLKLNDTV TGEDSVLDVT
AMFVAIGHDP RSEILAGQVE VDPSNYVLVQ EPSTRTNLDG VFAAGDLVDS HYQQAITAAG
SGCRAAIDAE HYLASLA
```

> RXA01433 (1-603, translated) 201 residues
```
MTVLPKNHDL SDTQLVKQFI SGDSRAFSTI IHRHERHMMQ AARKYGRKPE DAQDILQEAL
FRASRNMHLY RAEAALGTWL HKLVLNSGFD WATHRSQVEF PILNEPTIDL EKDPRLATDP
LGYLDVAMTI RSAIDQLHPD QRIALILVDL GGYTVEDVAE IEGIKVGTVK SRRGRARKAL
RALLHADFFG PEDGSIQCES N
```

> RXA01443 (1-831, translated) 277 residues
```
VLKINRSSYY KWKKTAPTRS NRLLSDAVLG AKIKSIFTKE RGCYGSKRIT AELNDDPGST
PVNHKRVARI MASLKLFGFT KKRRVITTVS DKKKPVFPDL VKRHFNALAA NEVYVGDITY
LPIADGTNMY LATVIDCYSR RLVGFAIADH MRTSLVQEAL LMAKSQRGSL KGAVFHSDHG
SVYTSQAFQD TCKKLGVRQS MGAVGTSADN SLAESFNAAL KREVLQDSKT FANQLVCRRE
VFRWCTRYST NRRHSWCGYV VPAVFESRNL AILKSVS
```

> RXA01444 (1-267, translated) 89 residues
```
MPTKTYSEEF KRDAVALYEN SDGASLQQIA NDLGINRVTL KNWIIKYGSN HNVQGTTPSA
AVSEAEQIRQ LKKENALQRA RTRHPAESC
```

> RXA01449 (1-1041, translated) 347 residues
```
LKLFISRALI AGTVSLTLFS SPLASAQSSG LSSVLSSEDS SATNSEQDFE KSSESGSSAQ
DFIALSTANP DLTGGSVEGL LSSMSLIGSS QLPLGGPLLS SDSNYPLETD PSITEARIVE
KRVLNGLRLE KWSVASPSMQ RNVDVQIMKS AEADSPAPML YMLDGIGGNK NSSGWINGGE
GPKVFADENV TVVMPLGAAS SMYSDWLEED PALGRIKWET FIVEELAPLL EAEEELNFNG
HRGIGGLSMG ATGAVHLANS NPDLFDGVIG ISGCYSTLDP IGQTTVSLIV NSRGGNVENM
WGPTGSETWK AHDVTSNPEG LRDMAVYLSA ANGVVDDIDL ADSEKEP
```

> RXA01490 (1-891, translated) 297 residues
```
MNAPAPKPGL VIVDKPAGMT SHDVVSKLRR AFSTRKVGHA GTLDPMATGV LVVGIERGTR
FLAHMVASTK AYDATIRLGA ATSTDDAEGE VISTTDASGL DHSTILAEIV NLTGDIMQKP
TKVSAIKIDG KRAHERVRDG EEVDIPARPV TVSVFDVLDY HVDGEFYDLD VRVHCSSGTY
IRALARDLGN ALQVGGHLTA LRRTEVGPFT LNDATPLSKL QENPELSLNL DQALTRSYPV
LDITEDEGVD LSMGKWLEPR GLKGVHAAVT PSGKAVALIE EKGKRLATVF VAHPNTL
```

> RXA01493 (1-1311, translated) 437 residues
```
MSMSNNDFEH ESHDVSAKQI FGLAFPALGV LAAMPLYLLL DTAVVGTLGG FELAALGAAT
TIQAQVTTQL TFLSYGTTAR SSRIFGMGDR RGAIAEGVQA TWVALFVGLG ILTLMLIGAP
TFALWLSGDE ALAQEAGHWL RVAAFAVPLI LMIMAGNGWL RGIQNTKLPL YFTLAGVIPG
```

```
AILIPIFVAK FGLVGSAWAN LIAEAITASL FLGALIKHHE GSWKPSWTVM KNQLVLGRDL
IMRSMSFQVA FLSAAAVAAR FGTASLAAHQ VLLQLWNFIT LVLDSLAIAA QTLTGAALGA
GTAKVARRVG NQVIKYSLIF AGGLGLVFVV LHSWIPRIFT QDADVLDAIA SPWWIMVAMI
ILGGIVFAID GVLLGAADAV FLRNASILAV VVGFLPGVWI SYALDAGLTG VWCGLLAFIL
IRLFAVIWRF KSMKWAR
```

RXA01496 (1-1728, translated) 576 residues
```
ADAAALVQAL FNLGEMVTAT ASVSDETLQL LGEEMNYKVQ VVSPEDEDRE LLESFDLQFG
EDEGGEADLA KRPPVVTVMG HVDHGKTRLL DTIRKANVGS DEAGGITQGI GAYQVKVNVE
DTERTITFLD TPGHEAFTAM RARGAKSTDI AVLVVAADDG VMPQTVEAIN HAKAADVPIV
VAVNKIDKPE ASPEKIRGQL TEYGLIPEEY GGDTIFVDIS AKQGLNIDEL LASVCLTADA
ELDLVANPEM DAQGVAIEAH LDRGRGPVAT VIVQRGTLRV GDSIVAGDTY GRVRRMVDEY
GRDVEEAGPS RPVQVQGLNG VPGAGDNLLV VEDDRIARQI ANQRNARKRN ALAARSRKRV
SLEDLDSVLK EHSTLNLILK GDNAGSVEAL EEALLKIEMD DEVQLNIIDR GVGAVTQTNV
TLAAASDAVI IAFNVRAEGK ATEEANAEGV DVRYYTIIYR AIEEVEAALK GMLKPIYEER
VIGHAEIRAI FKASSVGLIA GCMVEDGKVR RNATVRIIRD GNVIAENAKI VSLRREKDDA
TEVSAGYECG MVLSYPDISV DDKIEVYEMV EVPREA
```

> RXA01522 (1-1578, translated) 526 residues
```
VTNSNPTSKN NSADLPEQLR IRREKRERIL DSGLDAYPVE VDRTISISDL RSQFVVITED
LQEREEGVTY LEVGEETDVE VAIAGRVMFV RNTGKLCFAS IQEGNGTTVQ AMLSLAAVGE
ESLKAWKADV DMGDIVSVRG KVISSKRGEL SVMADSWHMA SKSLRPLPVA FADLSEDTRV
RHRYTDLIMR EQARTNALTR IKVMRALRHY LEDQDFLEVE TPMLQTLHGG AAARPFETHS
NALDIDLYLR IAPELYLKRC VVGGIERVFE VNRNFRNEGV DSSHSPEFAM LETYEAWGTY
ETGAKLIKGL VQSVAQEVFG TTLVTLADGT EYDLGGEWKV IEMYPSLNEA LARKFPGQPE
VTIDSTVEEL REIAKVIGLS VPENGGWGHG KLVEEIWELL CEDQLYGPIF VKDFPVETFP
LTRQHRTKPG VTEKWDLYVR GFELATGYSE LIDPVIQRER FEGQARLAAD GDDEAMVLDE
DFLTAMEQGM PPTSGNGMGI DRLLMALTGL GIRETVLFPM VKPEQK
```

> RXA01530 (1-642, translated) 214 residues
```
MAFLDLIQEG NLGLIRAVEK FDYSKGYKFS TYATWWIRQA ITRAMADQAR TIRIPVHMVE
VINKLGRIQR ELLQELGREP TPQELSKEMD ISEEKVLEIQ QYAREPISLD QTIGDEGDSQ
LGDFIEDSEA VVAVDAVSFT LLQDQLQDVL ETLSEREAGV VKLRFGLTDG MPRTLDEIGQ
VYGVTRERIR QIESKTMSKL RHPSRSQVLR DYLD
```

> RXA01531 (1-1017, translated) 339 residues
```
MVENNVAKKT VAKKTARKTA RKAAPRVATP LGVASESPIS ATPARSIDGT STPVEAADTI
ETTAPAAKAP AAKAPAKKVA KKTARKAPAK KTVAKKATTA KAAPATAKDE NAPVDDDEEN
LAQDEQDFDG DDFVDGIEDE EDEDGVEALG EESEDDEEDG SSVWDEDESA TLRQARKDAE
LTASADSVRA YLKQIGKVAL LNAEQEVSLA KRIEAGLYAT HRMEEMEEAF AAGDKDAKLT
PAVKRDLRAI ARDGRKAKNH LLEANLRLVV SLAKTLHRPW HGIPGPHPGR QPRSDSCRRE
VRLLQGLQVL HLRNLVDPSG NHPRHGRPST NHPYPSPHG
```

> RXA01541 (1-771, translated) 257 residues
```
IFNSHRAPRL ASTVIIARES ADSGTLEFFI QQRQSTMAYA ANAVVFPGGG VEDSDYPFML
PHRDQHMSPE HIKHHASRLH MDSETMAAHI SAARREVWEE TGVDLGNYNH ELIPIDRWIT
PDIPAFRRRY DTATFVLILS KDSTNAALQH QHQTTEATHS YWATAEELLT QWSTGHLNLL
LPTWWHINQL NHLHTLNQLY SFAQRTHNPQ HTPPTVFANW TAPADEAAMQ HYGFPDPDAY
FDHATIAGKH HTLITRK
```

> RXA01556 (1-849, translated) 283 residues
```
NIRFETLNIM GPARRIHLGH VWNDRLTFEY SRSLFGKETL SPDIARLFTD RVPTPPLPAP
RKARAVAQVL VSNPADQTSL EEFAEIQGVS ARTLQRQFLK STGYSFSEWR AAQRVCVAAS
LLAHDFSISV VANLVGFAAT SSLTRAFRRH TGATPSTFTT GQIGMGSAGH PPRIPATTTF
AEAHQDQQLW IYSGTATVTT PGYCRFMGQG DMVTIPAGTQ TRIDVAAGSI AFPVPVGLDE
WGMDLTRVVA VNNQQPKPLT ILEQSEWSKL SEELLNTPVP VQM
```

> RXA01558 (1-1209, translated) 403 residues
```
MTDSQTESLS TQSVKPAKKR SWFNSLYTGD GGIDFIAKTK LWYWITGILL VISILFIAIR
GFSLSIDFQG GTKMSMPASD YSTEQVEETF TEATGITPEI VQIVGSGDAR TLEIYSERLS
DEDVEKARLA IYEEYQPLNS EGQPSPDAIG NSTVSESWGS TITQRMVLAL IAFLVIAAIY
```

```
IAFRLEREMA IAAMAALVVD GIVIAGIYAV IGLEVSPATV IGLLTVLTFS IYDTVVVFDK
VRENTEGFEG SRRRTYAEQA NLAVNQTFMR SISTTIISAL PIIALMVVAV WMMGVGTLKD
LALIQLIGVI EGTFSSVFLA TPLLVSLKNR LSKTKAHTAS VMKLRDGQST LIDATPHTNA
DAFAHGTESD TDGVTPEAPA KRTVSKPIVD DHRSSGTWRP GRS
```

> RXA01559 (1-243, translated) 81 residues
```
ITAPLVILAS RNPFFAKSSV NGMGRVMKLV EERRANGELD EPEYLKKIHA KNAAADKAST
DNSSTDNSEA PGTDTNQEEE K
```

> RXA01582 (1-1089, translated) 363 residues
```
MAGLVDLTIN MREGLDYTVS EIQLTEASLN EAADAAIKAF DGAQNLDELA ALRRDHLGDA
APIPQARRSL GTIPKDQRKD AGRFVNMALG RAEKHFAQVK VVLEEKRNAE VLELERVDVT
VPTTREQVGA LHPITILNEQ IADIFVGMGW EIAEGPEVEA EYFNFDALNF LPDHPARTLQ
DTFHIAPEGS RQVLRTHTSP VQVRTMLNRE VPIYIACPGR VFRTDELDAT HTPVFHQIEG
LAVDKGLTMA HLRGTLDHLA KELFGPETKT RMRSNYFPFT EPSAEVDVWF PNKKGGAGWI
EWGGCGMVNP NVLRAVGVDP EEYTGFAFGM GIERTLQFRN GLSDMRDMVE GDIRFTLPFG
IQA
```

> RXA01583 (1-1716, translated) 572 residues
```
VETIEELTEF KKPIRHCHVN VGDANGTGEL QSIVCGARNF KEGDTVVVSL PGAVLPGDFA
ISARETYGRM SAGMICSASE LGLADKQNSG IITLDPSYGE PGEDARQALG LEDTVFDVNV
TPDRGYALSA RGLTRELASA FSLTFTDPAI EPAVAGIEVK VPAVEGSLIN VELREETKAI
RFGLRKVSGI DPAAESPFWM QRELMLSGQR PVNAATDVTN YVMLLLGQPM HAFDAAKVTG
DLVVRNATAG EKFETLDHVK RTLNEEDVVI TDDNGIQSLA GVMGGLTSEI SDTTTDVYFE
AATWDTITVA RTSRRHKLSS EASRRFERGV DPAIVEIALD IAATLLVEIA GGTVDAGRTL
VGDVPAMQPI TMKVTRPSEL AGVDYSAETV IARLEEVGCT VAVSGDTLEV TPPTWRGDLT
MSADLVEEVL RLEGLEAIPT IIPTAPAGRG LTDAQKRRRA VGHALAYAGY AEIIPSPFMD
PEVFDVWGLA ADDERRKTVS VLNPLEAERN VLSTSLLPSM LDAVKRNVAR GHNDFSLFGL
QQVAFEHGSG VSPMPSVASR PEESVVAELV DS
```
>
> RXA01596 (1-1779, translated) 593 residues
```
MLVDIAIENL GVIPAASAEF SSGLTVLTGE TGAGKTMVVT GLRLLSGGRA DASRVRTGSP
QAVVEGRFVT QGVPCDIVER ATGIVSNAGG AADENGEFLA VRSVGANGRS KAHLGGRSVP
AATLSEFSDE LLTIHGQNDQ LRLLSPERQL EALDRFDPEL AQLRKNYNAK YLTWKSLDKD
LQKRLSSRRE LAQEVDRLQF AINEIEEVSP QPGEDAELVE QIRRLQDVDT LREQAATALA
AIDGAGSLSD AMGGSGGFDE SQESASDQLG QAESALAGSD DSKLKDIAVQ LAEITSQLSQ
VSMELGGFLS DLPADPQALD DMLTRQQQLK LLTRKYAADI DGVIEWQRKA QIRLDSIDIS
SEALDKLKED AKKAQASMMR AAKKLSAVRA KAATKLGTTV TEELQGLAMQ KARFEVALTS
IEACASGIDQ VEFQLAANAF AQPRPLASSA SGGELSRVML ALEVILAAGT TGTTLVFDEV
DAGVGGRAAV EIGRRLARLA TKNQVIVVTH LPQVAAYADT HLHVAKNVGE ASVTSGVESL
TFDRRVEELS RMLAGLDDTA TGRAHATELL ERAQREKEDI NEERVEPLLA ASA
```

> RXA01601 (1-912, translated) 304 residues
```
MKARVLAKTW LTHLAVERGL SANTLSNYRR DVERYCDWLE AAGLDDIRDI TTAHVESYVK
DLRRGIDGQQ ALSASSAGRA LIVARGLHKF ALMEGEVAAD VAADVSPPAM GRHLPDTLSI
NEVALLIDAI PHSDIATPVD LRDRALVELL YGTGARISEA IGLAVDDVSE MPEVLRITGK
GSKQRIVPFG SMAQQAVREY LVRARPALSK GKSHALFLNQ RGGPLSRQSA WAVLKKTVER
AGLDKDISPH TLRHSFATHL LEGGADVRVV QELLGHSSVT TTQIYTHITA DSLREVWRGA
HPRA
```

> RXA01613 (1-1215, translated) 405 residues
```
MSEQPASIKH YDLIIIGTGS GNSIPGPEFD DKSIAIVEKG AFGGTCLNVG CIPTKMYVYA
ADIAQEIQES ARLGIDATVN SVDWPSIVSR VFDKRIDLIA QGGEAYRRGP ETPNIDVYDM
HASFVDSKTI STGIAGQEQL ISGTDIVIAT GSRPYIPEAI AESGARYYTN EDIMRLAQQP
ESLVIVGGGF IALEFAHVFE ALGTKVTILN RSDVLLREAD ADISAKILEL SKKRFDVRLS
TAVTAVHNKA DGGVKISTDT GDDIEADILL VATGRTPNGN QMNLDAAGIE MNGRSIKVDE
FGRTSVEGVW ALGDVSSPYK LKHVANAEMR AIKHNLANPN DLQKMPHDFV PSAVFTNPQI
SQVGMTEQEA REAGLDITVK IQNYSDVAYG WAMEDKDGFV KLNCR
```

> RXA01621 (1-1440, translated) 480 residues
```
VDQEVDRLAL MARAHQAIGE LSDILVPLAA AFSSKGHSLY LVGGSVRDAF LGELGHDLDF
```

```
TTSARPEETK AILDDYADVV WDTGIAFGTL SAEKHGQQIE ITTFRSDLYD GNSRNPEVTF
GDTLEGDLIR RDFKVNAMAV EIQADGELTF HDPVGGLEDL LTHTLDTPAT PEQSFNDDPL
RMLRAARFVS QLNFTLAPRV ITAMTEMAQQ ITRITVERMQ VELDKMILGK NPEAGIDLMV
ESGIAQIIYP EIPAMQMTQD EHMQHKDVYA HSLQVMRQAI DQEEDGPDLV LRWAALLHDC
GKPDTRDFNE EGRVSFHQHE VVGAKLVRRR MRKLKYSKQM VGDVGQLVFL HMRFHGFSEG
QWTDSAVRRY AADAGELLPR LHKLVRADCT TRNKRKAARL QATYDHLEER IAEIAAKEDL
ARVRPDLDGN EIMEILNIQA GPEVGKAWAF LKELRLERGP LDREVAIAEL KSWWEGENNE
```

> RXA01648 (1-369, translated) 123 residues
```
VGFAFADHMR TSLVQEALMM AKSQRGSLQG AVFHSDHGSV YTSQAFQDTC KKLGVRQSMG
AVGTSADNSL AESFNAALKR EVLQDSKTFA NQLVCRREVF RWCDLVQHGA QTFLVWLCGA
CGV
```

> RXA01649 (1-420, translated) 140 residues
```
VLKINRSSYY KWKKTALTRK KLLLSDAVLG AKIKSIFTKE RGCYGAKRIT AELNDGPGTT
TPVNHKRVAR VMSSMKLVGF TKKRKVITTI PAAVKPVFPD LVKRQFNALA ANEVYVGDIT
YLPIADGSNM YLTTVIDCYS
```

> RXA01650 (1-114, translated) 38 residues
```
MSEAEQIRQL KKENALLREE RDILRKAAKY FPGKRQDL
```

> RXA01651 (1-135, translated) 45 residues
```
MPTKTYSEEF KRDAVALYEN SDGASLQQIA NDLGINRVTL KNFDQ
```

> RXA01670 (1-612, translated) 204 residues
```
HFVYHLGLIG TLQFEPAEET RGQIRLHLSD GEIAANLRGP QWCRLITDAE RTQAIGKLGA
DPIRDDADPE PIRIKVQRSG RSIGSLLMDQ KLFAGVGNIY RAETLFRLGI SPFTIGKDIT
TAQFRSIWAD LVGLMKDGVV TGRIDTVRPE HTPEAMGRPP RKDDHGGEVY TYRRTGQECF
LCATPIKEQV MEGRNLFWCP GCQR
```

> RXA01680 (1-411, translated) 137 residues
```
MAGHTHKTHR TAYKQLEALA RNGHLFTYID PPAEVDGVVK STTNCLEGGI NAQIKALARN
HRGMFDEHQR IAVDWWLLMH TQLPGDPDEI ARQQNWGQDG LANVPDLIQQ EQPHDHYGRP
VTYDTGIDAT TTRRKSK
```

> RXA01704 (1-816, translated) 272 residues
```
DASGRAGFRK LKSNELVTEV ACSQVVPELL EGLVGEGARR FTPGVEIIAA IDDAGQRHVV
ESRKAPRGRR TETVLKVLEG TGEVEQKVGD YTWKFPVSSF WQAHTKAPAA YSEFIAEALT
GLELVDVDKR GPVAWDLYGG VGLFAPIITS KLQAAVHSVE LSPGSAEAGE EALAGLPVTF
HTGRVEGMAS QLPSPNVVVL DPPRTGAGSD VLKSIAEAKP QLVIHIGCDP ATFARDVADW
KLNGYEMDQL AVFNAFPGTH HFETIGVFVR VS
```

> RXA01710 (1-408, translated) 136 residues
```
MTDFKLISDT EWRERLTPQE FHVLREAGTE PPHVGEYTNT TTEGVYSCRA CGEELFRSTE
KFESHCGWPS FFSPLAGDKI IEKEDLSLGM RRVEILCANC GSHMGHVFEG EGYDTPTDLR
YCINSISLKL EEKPVS
```

> RXA01717 (1-282, translated) 94 residues
```
PSQQMHQDIA LVVDETIPAE DVRAVVKAGA GELIETVELF HVFRSEQRGE NKKSLAFSLR
FRAAGRTLTD EEANEARLQA AELAKEKFNA EMRG
```

> RXA01723 (1-837, translated) 279 residues
```
VDXSRVTTTA TTPEPAAPAQ SQPAEAQPAQ TQAAQQEELP VAAKESAPAT ENTQGQXQGQ
AQGXAQGDEH DDXFESRSAA RRARRNRQRQ IHRDGDDNAN ANTESEQNTP AQNATAQAES
EQTAAPAQAE AAEQNQNDNS ESSENRSDNY RNNNRRSRNN RNNRNYRDNN ESSDNAGQSS
NDDADNNQAR SEDNNDDRRS RNNRNNDRND RNDRNDRDND DNDDRRNRRG RRNRRGXATT
VTIATTEITG ITATTATMAT TTSKXEXAAG SRHPGHRGP
```

> RXA01724 (1-384, translated) 128 residues
```
VDHNVAFVRT TGYHAAPSDV FVSNQLIRRM GLRSGDAIEG QVRMNQGGGN HNNHGRNRQK
YNNLVRVEMV NGLPAEETRN RPEFGKLTPL YPNQRLRLET EQKILTTRVI DLIMPIGKGQ
```

LCFDCVAT

> RXA01725 (1-108, translated) 36 residues
LVDERPKEVT DMQRSVNGEV ISSTFDRPPS EHTAVA

> RXA01726 (1-573, translated) 191 residues
LLELAIERAK RLVEQGQDVV VLLDSITRLG RAYNNSSPAS GRILSGGVDS NALYPPKRFL
GAARNIENGG SLTIIATAMV ETGSAGDTVI FEEFKGTGNA ELKLDRKISE RRVFPAVDVN
PSGTRKDELL LNPDEARIMH KLRRILSALD NQQAIDLLIK QLKKTKSNAE FLMQVASSAP
MAGTEKEEDY S

> RXA01730 (1-1677, translated) 559 residues
VLRTHLSGEL RKENAGQSVT LTGWVNRRRD HGGVIFIDLR DRTGIAQVVF RNEDVAERAH
ALRSEFVLRV TGVVEERPEG SQNPNLASGD IEVSVTEFEV LNESAPLPFQ IEDSSSAGEV
GEETRLKYRY LDLRRPVQAN ALRLRSAANK AARTVLDSHD FTEIETPTLT RSTPEGARDF
LVPARLRPGT FYALPQSPQL FKQLLQVAGM ERYYQIARCY RDEDFRADRQ PEFTQLDVEM
SFVDQDDVIA LGEEIISEVW KLIGYEIKTP IPRMTYADAM RRYGSDKPDL RFDIEITECT
EFFQDTTFRV FKNEYVGAVV MTGGASQPRR QLDAWQEWAK QRGAKGLAYI LVGEDGELSG
PVAKNITDAE RAGIAAHVGA QPGDCIFFAA GDTKSSLALL GAARGEIAKK LDLIKEGDWA
FTWIVDAPMF EPAADATASG DVALGNSKWT AVHHAFTSPK PEFLDNFDTN PGDALAYAYD
IVCNGNEIGG GSIRIHQRDV QERVFEVMGI TGEEAREKFG FLLDAFAFGA PPHGGIAFGW
DRIVSLLGGF DSIRDVIAF

> RXA01733 (1-543, translated) 181 residues
GPKIYEAYTT IAPESRPAAV NYKTTIDQGL SQFSEFDAGI IEATLLTELA AKRQREIERG
SSLVGPHRDD VDLMLGDQPA KGFASHGETW SFALSLRIAE FNLLKSDGTD PILILDDVFS
ELDAGRREKL VGIAQEVEQV LITAAVHDDL PENLKKVLTA QHTVTVQDTG TGRISLLDVQ
P

> RXA01784 (1-549, translated) 183 residues
TTIYRWVQKY ALELDKQTRW YRQVPDWQAS SWRVDETYIR VGGTWCYLYR AITAGGQTLE
FYLSPKRNVA AAKRFLAKTL RSNTTAGSPR VINTDKAPAL AKAISELKAE GICPQTVEHR
QVKYLNNVIE GDHGRLKRIL GPKGAFKNRI SAYRTLKGME AMHSLRKGQG TMFDLTGTRT
QTR

> RXA01798 (1-273, translated) 91 residues
MHRKKEELTM RKGISRILSV AVASSIGFGS VLSGTGIAAA QDSAFDYGMD PSMNYNPIDD
MKDRPQGLSN LPYFGSKLTS WGSSDATASS G

> RXA01818 (1-987, translated) 329 residues
MGYPIGGEVP VSGSNLIDGE INGWVQTFQG GRVYRTPMLE GFQIASINGM ILNRWLAIGG
PDSALGFPIA DEAVASDGVG RFSVFQNGVL YWHPNHGAWE MTGFIEEVWK MRGGLDSQWG
YPTSAPVLDS DAPVEIAQNF SGGVFDLATE IEDAGFSPIE DKEMSNLILE YFGYLGFDFP
GSSSRELVQD HSKSDLMTLR ASRCALKDSS QASFGGVTIP SHYDYWGCLD KSDRPDPDAY
GRHDYCTLSP DSYGPLGKKA EFSGACARHD LCMDAVDANG TGYAPCHPAF YTWMSTVCTT
NYAEDANFKK GCVNTAKAYY KAVQLKNPN

> RXA01819 (1-447, translated) 149 residues
LILPVQEGIS YFPTPLHLNH IGGSRFKKFL VKIDKTVPQD LDVHVICDNY ATHKHPTINT
WLVKHPRFHM HFTPTYSSWI NQVERLFAEV TRELLQRSDH RSVQALEKDL RNWVKAWNED
PKPFIWTKTA EEILSSIARY LKRINGAGH

> RXA01837 (1-393, translated) 131 residues
SEGYYNDTVC HRITTSGIYV LQCGDPSSTG AGGPGFSFAN EYPTDEATDL TTPVIYERGT
IAMANAGADT NGSQFFLNYE DSPLAPNYTY FGQITEEGLA TLDAIAEVGT EGGTGDGAPA
QEVRIESAAV A

> RXA01841 (1-363, translated) 121 residues
MEEGEEISLS DFEGEVVVLN AWGQWCAPCR AEVDDLQLVQ ETLDPLGGTV LGINVRDYNQ
TIAQDFKLDN AVTYPSIYDP PFRIAAALGG VPTSVIPTTI VLDRSHRPAA VFLREVTALS
G

> RXA01852 (1-1287, translated) 429 residues
```
VSQNKSKSEK LQSFAAPKGV PDYAPPKSAA FLAVRDAFVN QAHKAGFEHI ELPIFEDTGL
FARGVGESTD VVSKEMYTFA DRGERSVTLR PEGTAGVMRA VIEHSLDRGQ LPVKLNYAGP
FFRYERPQAG RYRQLQQVGV EAIGVDDPAL DAEIIALADR SYRSLGLQDF RLELTSLGDR
HCRPEYRQKL QDFLFALPLD EETRKRAEIN PLRVLDDKRP EVQEMTADAP LMLDHLDAEC
REHFETVTGL LDDMGVPYVI NPRMVRGLDY YTKTCFEFVH DGLGAQSGIG GGGRYDGLMA
QLGGQDLSGI GYGLGVDRTM LALEAEGVTV GAERRVDVYG VPLGKDAKKA LAGIVNTLRA
AGISTDMSYG DRGLKGAMKG ADRSNALYTL VLGEQELENN TIAVKDMRAH EQHDVALDEV
VAFLQGKLI
```

> RXA01862 (1-1206, translated) 402 residues
```
MAYDFVIGMD VGKYFHHACV LDPQGRQVLS KRINQHEGSL RKLFDKFLAN DAEVLVVVDQ
PNNIGRLTVA VAQAMGADVR YLPGLAMRQL SRIHVGNSKT DVRDAYVIAH AGLNLPDALR
SVDRVEEVFL QLKVLNGIDE DLARAYTRLI NQMQSALVGT YPAFEHVLRG QMIHRKWILH
LLAKYGGPTK IRRVGKARLA AFARGHRARN PEPVIDAMLA AIHGQTVSIA GAEYAELGVA
MSAKDALAKL EHRKEIEGQV LELIQDIPQT EILLSMPGIG PRSAAQILMT VGDMSDFPDA
AHLASYAGLS PQTNQSGTSI MSNSPNRAGN KKLKNALWQS SFASIRFHER SRQFYERKRN
EGKRHNAAVV ALARRRLNVL FAMMRSGELY RDIPTAQEAA AA
```

> RXA01863 (1-807, translated) 269 residues
```
MNSNLTLPQD RYLDIAEYID VMHISHNWGT TDEFANVGFG AMKKQPPLKA KLKLYEQMIS
NARTLSEQGM FVSAETMLNQ STLPHLRKIH QEVVHDMKCS RHEIHPMYPA DFASQLNVLT
LAEMKKTIHD ILDFRDEDIW MLFGTLPVFP CLKDDEDQKL LSRLRNANNV TTRNDPDGRS
RLNVNVFTGN VIVTDFGDET GTISNIQKDK LTDVFDKWLS SDLAKSLNCH CSEFSCLGPN
VLVKNMYYPN MDFKDNERHM HKQPQIIQF
```

> RXA01864 (1-471, translated) 157 residues
```
NERYWTGPRP ETHGPNDPGG VDLYVGGVEH AVLHLLYARF WHKVLFDLGH VSSKEPYRRL
YNQGYIQAFA YTDSRGVYVP ADDVEEKDGK FFYQGEEVNQ EYGKMGKSLK NAVAPDDICN
NFGADTLRVY EMAMGPLDTS RPWATKDVVG AQRFLSV
```

> RXA01872 (1-765, translated) 255 residues
```
MGNDGGDLRI DDLRSFISVA QSGHLTETAQ'RLGIPQPTLS RRISRVEKHA GTPLFDRAGR
KLVLNQRGHA FLNHASAIVA EFNSAATEIK RLMDPEKGTI RLDFMHSLGT WMVPELIRTF
RAEHPNVEFQ LHQAAAMLLV DRVLADETDL ALVGPKPAEV GTSLGWAPLL RQRLALAVPA
DHRLASFSGQ GELPLITAAE EPFVAMRAGF GTRLLMDALA EEAGFVPNVV FESMELTTVA
GLVSAGLGVG VVPMD
```

> RXA01878 (1-879, translated) 293 residues
```
MEEPSGAQLL GPVEIRALAE KLDVTPTKKL GQNFVHDPNT VRRIVAAAEL TPNDHVVEVG
PGLGSLTLAL VESAASVTAV EIDPRLAAEL PETFQWRAPA LAHKLSIVLK DALKVQQSDM
AVQPTALVAN LPYNVSVPVL LHMMEEFPTI NKVLVMVQAE VADRLAADPG SKIYGVPSVK
ASFYGPVTRA GSIGKNVFWP APKIESGLVK IVREDTAWKQ DDETRKKVWP IIDAAFLQRR
KTLRAALSGH YGSGQAAEEA LRAADIDPTL RGEKLDVTDY VRLAGVLQQK DEK
```

> RXA01913 (1-825, translated) 275 residues
```
MANYTAADVK KLRELTGSGM LDCKKALEES AGDFDKAVEI LRVKGAKDVG KRAERNATEG
LVAVSGNTMV EVNSETDFVA KNSDFKEFAA KVADAAAAAK ANSQEELAAV DVDGQTADAA
LQEFSAKIGE KLELRRAVTL EGDKTAVYLH QRSADLPPAV GVLVAFTGEG EAAEAAARQA
AMQIAALKAS YLTREDVPAE IIEKERSIAE QITREEGKPE QAIPKIVEGR LNGFYKENVL
LEQSSVADSK KTVKALLDEA GVTVTSFARF EVGQA
```

> RXA01926 (1-672, translated) 224 residues
```
LRSFYTPEQA IEREGDVWKA ATEEAELLAA DGAVHDQELF LNCTTSPLIF ASAMLNFGVH
QILDTLCQLA PSPAGRDADP KALEAATSAM DDHRDTTDDF SGVVFKVQAG MDKNHRDTLA
FMRVVSGEFD RGMQVTHSQS GRSFSTKYAL TVFGRTRSTV ETAFPGDIVG LVNAGALAPG
DTIFEGRKIQ YPPMPKFAPE HFRILRAKSL GKYKQFRKAL EQLD
```

> RXA01938 (1-915, translated) 305 residues
```
LDESYAKHRA AYQRIFDRLG LEYAICQATS GAMGGSASEE FLAVSENGED TFVRSTSGNY
```

```
AANVEAVVTQ PGVERDIEGL PEPVTYETPV SETIDALVDW ANSIDVQIEG REVTADDTLK
CIVVKVREPG AEEAELTGIL LPGDREVDMK RLEASLEPAE VELAVESDFA DNPFLVKGYV
GPVGLAKNGV KVLADPRVVT GTSWITGADE KERHVVGLVA GRDFTPDGFI EAAEIKEGDP
APAGEGTLTL ARGIEIGISS SSAASTPKPS TSKSWTKTAS APSQPWALRA RCHPPARRPG
RTAPR
```

> RXA01953 (1-381, translated) 127 residues
```
MIAAYREKDR SLGRAAMEAL IDAVSQDVPA GLDELRKLGR TLKARATDVL AYFERPGTSN
GPTEAINGRL EHLRGSALGF RNLTNYIARS LLEFRRIQTS TTPSSVKSRF RHPSSSRTTM
NDVPTHL
```

> RXA01954 (1-840, translated) 280 residues
```
VLADDVVVVA EFRDRIYPGL VETGRVERGG DKPFHTVVNA ENYHALEMLT YTHRHSIDAI
YIDPPYNTGA RDWKYDNDYV ASDDDYRHSK WLAFMERRLK ICRELMRSDA TLVAPIDEHE
VNRLGVLLDQ LFPESTRQLV TIVNNPKGVT QGYLSRVEEY AFFVFGPDAR IGSVDDDLLT
HRDMADAEGE LQRPRWKGLL RSGDDSLRAD RKDMFYPVWF DESTGRLSHA GEALPLDETP
DFSPQDGLTP IWPIRRDMKE GPTRAAPRRS ILDYALHPHL
```

> RXA01975 (1-1896, translated) 632 residues
```
LSHHTHLNNY ITSLSDNADL REKVTATVDA FRHTVMDDFD YISDQQVLLY GDVQSGKTSH
MLGIIADCLD STFHTIVILT SPNTRLVQQT YDRVAQAFPD TLVCDRDGYN DFRANQKSLT
PRKSIVVVGK IPAVLGNWLR VFNDSGALSG HPVLIIDDEA DATSLNTKVN QSDVSTINHQ
LTSIRDLATG CIYLQVTGTP QAVLLQSDDS NWAAEHVLHF APGESYIGGQ LFFSELNNPY
LRLFANTQFD EDSRFSDAIY TYLLTAALFK LRGESLCTML IHPSHTASSH RDFAQEARLQ
LTFAFERFYE PMIQHNFQRA YEQLAQTDSN LPPLRKILNI LGGMEDDFSI HIVNSDNPTV
EEDWADGYNI IVGGNSLGRG LTFNNLQTVF YVRESKRPQA DTLWQHARMF GYKRHKDTMR
VFMPATIAQT FQEVYLGNEA IKNQLDHGTH INDIRVILGD GVAPTRANVL DKRKVGNLSG
GVNYFAADPR IKNVEALDKK LLAYLDKHGE DSTIGMRAII TILNAFTVDP NDLDLATFKA
ALLDFERNQP HLTARMVLRT NRKVNQGTGA LLSPTDQALS RAEVAHPLLI LYRIEGVNDA
AAQRGEPTWS SDPIWVPNIK LPGQRQFWCV DG
```

> RXA01998 (1-708, translated) 236 residues
```
MGIFSGRQFP REIILWAVRW YCRYGVSYRD LEEMMTERGV PVDHTTIYRW VQKYAPELDK
KTRWYRQVPD WQARSWRVDE TYIRVGGKWC YLYRAITAGS QTLDFYLSPK RNVAAAKRFL
AKTLRSNKSA GYPRVISTDK APSLARAISE LKAEGVCPST VEHRRVKYLN NVIEGDHGRL
KRILGPKGAF KNRTSAYRTL KGMEAMHSLR KGQGTMFAYG HPNPDAVIVS RVFETA
```

> RXA02002 (1-378, translated) 126 residues
```
MSNANPDTTA AEAHRRRTFA VIAHPDAGKS TLTEALALHA HIISEAGATH GKAGRKATVS
DWMEMEKDRG ISIASSALQF EYAPEGHAGE PFMINLVDTP GHADFSEDTY RVLMAVDAAV
MLMHSV
```

> RXA02015 (1-519, translated) 173 residues
```
VLKFSLNLLD DIRPRAMSRD IDWGIPIPVE GWQDNNAKKL YVWFDAVVGY LSASIEWAYR
SGDPEAWRTF WNDPETKSYY FMGKDNITFH SQIWPAELLG YAGKGSRGGE IGDLGVLNLP
TEVVSSEFLT MSGSKFSSSK GVVIYVKDFL KEFGPDALRY FIAARPRNND TDF
```

> RXA02025 (1-651, translated) 217 residues
```
MAWFFAPEPV MVTADEALKG GRHPVLENPA PHTVLGTPVT GPWKEGQQRI WIGLGCFWGV
EQMYWQMDGV EGTSVGYAGG FTPNPTYREV CSGRTGHTEI VEVVYDPSKI SLEQLVARGL
EAHDPTQGFR QGNDVGTQYR SAYYTENEED AARVKAVVDA YGETLKQHGF GEITTEIGVI
SPSDYFLAED YHQQYLDKNP DGYCPHHSTG IPCGVEA
```

> RXA02047 (1-192, translated) 64 residues
```
WDDRVHPAHA RLFAQALLDA GQAVDYYENT EGGHAGAADN KQTAFVESLI YTWIEKTLDQ
QGSI
```

> RXA02065 (1-648, translated) 216 residues
```
MTYMKKKSRD DAPVVIETVQ AEHAEELTGT AAFDAGQADM PTWGELVAEH ADSVYRLAYR
LSGNQHDAED LTQETFMRVF RSLKSYQPGT FEGWLHRITT NLFLDMVRHR GKIRMEALPE
DYERVPGNDI TPEQAYTEAN LDPALQAALD ELSPDFRVAV ILCDVVGMSY DEIAETLGVK
```

```
MGTVRSRIHR GRSQLRASLE AAAMTSEEVS LLVPTH


> RXA02078 (1-858, translated) 286 residues
VPELPEVEVV RRGLEDHMVG HTIVSATVLH PRAARNQLGG GPEIEANIAG LRVSAAKRRG
KFLWLELIDA PSGETRPDLG LLVHLGMSGQ MLIKEPDAPI SPHLRAKVEL DNGDEVWFVD
QRTFGYWWLG DLVDGVPERV SHIATDVLDE SADFSAIARN LKSRKSEIKR LLLNQEIVSG
IGNIYADEML WQAKIHPLQR ADRLSLARLE ELLQAGKDVM TKALAQGGTS FDALYVNVNG
NSGYFALSLN AYAQTGEPCG RCGTLIIRES FMNRGSHYCP NCQKRR


> RXA02110 (1-618, translated) 206 residues
MAVSTIIFAL RPGPQDLPSL WAPFVPRTRE PHLNKWALPG GWLPPHEELE DAAARTLAET
TGLHPSYLEQ LYTFGKVDRS PTGRVISVVY WALVRADEAL KAIPGENVQW FPADHLPELA
FDHNNIVKYA LERLRTKVEY SEIAHSFLGE TFTIAQLRSV HEAVLGHKLD AANFRRSVAT
SPDLIDTGEV LAGTPHRPPK LFRFQR


> RXA02130 (1-87, translated) 29 residues
MTSDLQSRRR LGLTATLVRE DGREGDVSA


> RXA02167 (1-1260, translated) 420 residues
MNIIDELSWR GLINQSTDLE ALREEASTPI TLYCGFDPTG PSLHAGHLVP LLMLRRFQQA
GHNPIVLAGG ATGMIGDPRD VGERTMNSAD TVSDWAERIS GQLSRFVDFD GEHAARLVNN
AEWTNEMSVV TFLRDVGKHF SLNTMLARDT VKRRLESDGI SYTEFSYMLL QANDYVELNK
RFGCTLQVGG GDQWGNIVSG VDLNRRVNGT SVHAVTVPLV TDSDGKKFGK STGGGSLWLD
PEMTSPYAWY QYFINASDAD VIRYLRWFTF LTQEELAELE VEVAERPFKR EAQRRLAREM
TNLVHGTEAT EAVELAAQAL FGRAELRDLD EKTLAASVSE TAVAEIKAGE PRTIIDLLVA
SGLADSKGAA KRAVKEGGAY VNNERIESDD WEPFAEDLLH GSWLVLRRGK KNFAGVQILG


> RXA02174 (1-354, translated) 118 residues
MEKPQIELPV GPAPEDLVIS DIIVGEGAEA RPGGEVEVHY VGVDFETGEE FDSSWDRGQT
SQFPLNGLIA GWQEGIPGMK VGGRRQLTIP PEAAYGPEGS GHPLSGRTLV FIIDLISA


> RXA02182 (1-774, translated) 258 residues
VKKLASIAIL SSLPLASCST PPTDSEAVVE HLVPEIISTH SFDSTSFTQG LELDGDELIV
GTGQYGGSRI YRSSVDGQES VSQSLDPEFF GEGITKSGDA IWQLTWNEGV AFKRDADTLE
ELDRVSYNGQ GWGICSTDDA LITSDGSSTL TFRDPETFAE NSTVDVTLDG SPVGNLNELE
CVDGEVYANI FLDTDIMRID PNSGEVTAVI DASNIPNNAT PDTNNVLNGI AHIPDSDRFY
ITGKRWPDLY EVRFVPAD


> RXA02204 (1-1260, translated) 420 residues
MQSWPTPEVP ALAGTPVPLE LFDTADQEVR LVETPPAGSD TPVGMYVCGI TPYDSTHLGH
AATYLAFDLI YRILLDNDHD VHYVQNITDV DDPLFERAAR DGVDWRDLGT SQINLFRSDM
EALSIIPPKD YIGAIESIDE VIEMVKTLLD EGAAYIVEDA EYPDVYASIN ATDKFGYESN
YDAATMAEFF AERGGDPERP GKKNPMDALL WRAAREGEPS WESPFGAGRP GWHIECSAIA
TNRLGHSFDI QGGGSDLIFP HHEFSAAHAE AAHGVERMAK HYVHAGMISQ DGVKMSKSLG
NLEFVSRLTA AGHEPGAIRL GVFANHYRGN RDWNAESLAT AEQRLATWRE AARAATNRED
AIAVVEQLRA HLSADLDTPG ALAAVDNWAA GIDTTTDSKE FTEVGNIVVA AIDALLGVQL


> RXA02228 (1-903, translated) 301 residues
VVTPIAVVGP TASGKSALGI ALAHKLDGEV VNVDSMQLYK GMDIGTAKLT VEEREGIAHH
QLDVWDVTET ASVARFQSDA VADVEDIMSR GKTPILVGGS MLYVQSLVDD WQFPPTDSAV
RARFEARLAD IGVEALHAEL TQLDPEAAAV IESNDPRRTV RALEVIELTG QPFQASQPPK
DAPPRWGTRI IGLKTTPEWL NPRIEQRTAR MFEQGFVAEV EHLVQQGLIA DSTAGRAIGY
SQVLAAMAGE MTWEDAFERT VTGTRRYVRR QRSWFNRDHR VSWVDASGDP TAQALEILGL
Q


> RXA02236 (1-318, translated) 106 residues
VALPQLTDEQ RKAALAKAAE ARKARAELKE NLKRGNTNLR EVLDKAESDE IIGKTKVSAL
LEALPKVGKV KAKEIMDELG IAQTRRLRGL GDRQRRALLE RFGFED


> RXA02242 (1-507, translated) 169 residues
MAVREVRLFG DPVLVSRADE VVDFDESLST LIDDMFDTME DAGGVGLAAN QVGVLRRVFV
```

```
FDTSHQEGGL RGHVINPVWE PLTEDTQTGK EGCLSIPDVS AETTRYETVR LSGQDRDGNP
VGFVANGLLA RCIQHETDHL DGVLFLKRLD PAERKAAMGV IRASAWFNK
```

> RXA02243 (1-945, translated) 315 residues
```
MRLVFAGTPE PAVVALQKLI DSDHEVVAVL TQPDARRGRG RTLHPSAVAE LAQQHGIEVL
KPTSLKADTE DGQAIRQRLA ELAPDCLPVV AYGQLITKDL LDVAPHGWVN LHFSLLPAWR
GAAPVQASIR EGDQITGATT FRIDEGLDTG VILSTIEDTI QPTDTADDLL TRLAYSGGDL
LVETMTGLEQ GTITPRAQEG EATYASKITT QDAQIDWSKP AEVIDRHIRA HTPGPGAWTT
LVDARLKVGP ISHSGEVEVA ADLAPGAILA QKNSVVVGTG TTPIVLGNIQ PPGKKMMNAA
DWARGVQLDQ EAKFQ
```

RXA02251 (1-300, translated) 100 residues
```
VADPTTYRPA PGTIPTEPGV YKFRDENRRV IYVGKAKNLR SRLSNYFQDV TQLHPRTRQM
VFAASSVEWT VVSSEVEALQ LEYTWIKRFD PRFKRKIPRR
```

> RXA02252 (1-1824, translated) 608 residues
```
LIRGSNVKYR DDKTYPMLAV STGERFPRAF FFRGPRRKGV RYFGPYSHAW AVRETLDLLT
RVFPMRTCSK GVFNRHESLG RPCLLGYIDK CAAPCVGRVS EEEHREIVDG FTSFMAGHTD
KVTRKLNADM MAAAEELDFE RAARLRDDLE AIDKVMEKQA VVLGDGTDAD IIAFATDQLE
AAVQVFNIRG GRIRGQRGWV VEKPGDYAGL LVDATTQPEG DAPETDPALP FLMQDFLVQF
YGDAVERAET EAKEDAAVIE RRGVDKHSFE EAAPVTRASV VPREILVQVA PNEAEQTLKV
LEELRGAGVD ARVPQRGDKR ALMETVERNA KELLKQHKLK RVGDLTARSA ALQELQEALD
MEQAPLRIEC TDISHIQGTD VVASLVVFED GLPRKSDYRR YRVKEAAGDG HSNDVASIAE
ITRRRFLRHN QDKLAVPEAE EFDGSTFSDE KVEEMSTDAR RFAYPPQIFI VDGGAPQVAA
AQEVFDELGI VDVVLIGLAK RLEEIWLPGD PDPVILPRNS QALFLLQQIR DEAHRFAITY
HRQQRSKRMR VSELDSIKGL GQSRRTELVK HFGSVAKLKE ASVEDISQVK GFGPKLAEAV
YEGLHASK
```

> RXA02260 (1-231, translated) 77 residues
```
MALTLQIILV VASLLMTVFV LLHKGKGGGL SSLFGGGVQS NLSGSTVVEK NLDRVTILVA
VIWIVCIVAL NLIQTYS
```

> RXA02290 (1-399, translated) 133 residues
```
VDLNALFEIL TLVVFQVGVT WHAVLSKREG FRQAFAQFDV AKVAAFNEDD VERLLDDLQI
FRNRRKINAA ITNAKALLEL NDETGTFDSI IADHSTDATA MVKHLKALGF THIGLTSLSI
LQQAIGVTEL KAA
```

> RXA02291 (1-654, translated) 218 residues
```
VVHLPNFLGL AEQKALVAQA RDLAREVVGT PLAMVRPKLK SGQMSVHMLH LGKYWASNPY
RYVDVVDGFP VPPLPDSFVD LAHRALLSAG SLSNSLQSWS EAYRAEAALV NYYSPDASMG
MHQDANEESE APVISLSIGD TGIFRLGGTL NRNKPWTDIP LMSGDLIVFG GANRQAFHGI
PSIEANTAPA GCGLKEGEST SRSANLHYKT PGRGMSRG
```

> RXA02323 (1-924, translated) 308 residues
```
MSSHDLVDVV VVGAGAAGLA AAVALGRSLR SVIVIDAGQP RNSYAHAAHN VLGQEGIAPA
ELLEKGRAEA RSYGVTIAPG RVAKVERTGS TFAITLDDAS LLHSRRIILA HGAVDDLPEV
EGLSDFWGTK VLHCAYCHGF EARDSEIVVV GTSPMAAHQA LMFSQLSKTV SLVGTIDIDE
QTSESLDSAG VKVLGTNAVR VSAEGDGLSV ELSEGDHLSC DNIVVASRPL VDGTLYTQLG
GQMEENPMGR FIPGTQTGRT PIEGVWAAGN AQAPMAMVYG SAAQGVMAGA EINFDLILED
ISVASAQS
```

> RXA02385 (1-771, translated) 257 residues
```
MIEVRLVPVA AVMWMAVAAL IINGSWVLSV GIVGIAIIAA CVFKHWGQAV VIAALGVGAV
VMAALRISSA KAFEAPQTWV GTAETIKFLD SGDQLIGLRV EGYPAPIPVF YSGSDTIEKA
SLIAVSGRIK PDSFPGVGDL TISTEDIDQL EPTTGYSAWV NQVRDGFSQA VEETVGESSR
GLIPGMVLGD TRLQGSIEAQ TYIDTGLSHL SAVSGSNVAI VVSSVVVLSY FLTAGPRIRV
VASLLSLGIF VSLVGFE
```

> RXA02386 (1-405, translated) 135 residues
```
VSVVGHVAKP GLVTLAEGSR VADALAIAGA LPDADLTALN LAQLLVDGTQ IHVLAIGEVQ
PISVDAAATS ASGLISLNTA TVADLVTLPG VGEKTAQAII DFRESNGGFS TVEDLLQVKG
```

IGPSKFEQIS GLVSP

> RXA02388 (1-846, translated) 282 residues
AIINSSRMEP MHGLSLSVIC LLFYDSNLAV HYGFLLSCAA TAGIVMLQPL LYRAIGPPLA
VWKVPDIVVR AFAVSIAADL VTIPIIALMA RQISLVAVLA NVLVELAVPP ITLLGLIAVL
ASLLPWPVEY PLLKIIEPFT WWIHHVAKWC QQLPNSTLEI SAGWAGIAWA CMAAVWVVVI
IYKGYVRTLA VCCVCFFLFG AWNNRLPAQI DPTELRFVII ADDSELTDVP EHAELIIVED
PHGSMSDRPI VTREGIPVLY PYRDGEVSLH IDGTQHAADG RF

> RXA02413 (1-492, translated) 164 residues
MTSENSESQD IWLTDEQQDV WLDVWTMRIG LPARLDAQLK EAAGVSHFEY FTMAQISMAP
EHRVRMSELA ELSDMTLSHL SRVVTRLEKA GWVKRVPDPD DGRATVAVLT DSGWEKVKAT
APGHVKEVRR LVFDDLTPEE LKVMGTAMKK IVNRLDMSNR LPRV

> RXA02416 (1-2640, translated) 880 residues
DKPDVDLIDG LSPAVSIDQK STNRNPRSTV GTITEVYDYL RLLYARAGTA HCPVCDARVE
RQTPQQMVDQ ILGMEEGLKF QILAPVVRTR KGEFVDLFAD LASQGYSRVR VDGEVHQLSD
PPKLEKQIKH DIDVVVDRLQ VKASQKQRLT DSMETALRLA DGVAVLEFVG LEEDDPNRLR
RFSEKMSCPN GHALTVDELE PRAFSFNSPY GACPACDGLG VRTEVDIDLI IPDPDAPATK
AVQPWNSSPN HSYFEKLIEG LAKALGFDPE TPYSELTAAQ KKALVYGSKE EVSVRYKNRY
GRVRSWTAPF EGVMGYFDRK LEQTDSETQK DRLLGYTREV PCPTCKGARL KPEILAVRLD
SGSHGALSIA GLTALSVHEA FEFLDNLTLG KREEMIAGAV LKEIHARLKF LLDVGLSYLT
LDRAAGTLSG GEAQRIRLAT QIGSGLAGVL YVLDEPSIGL HQRDNQRLIT TLEHLRDIGN
TLIVVEHDED TIRRADWLVD IGPRAGEFGG EVVYQGEPKG ILDCEESLTG AYLSGRRTLG
VPDTRREIDK ERQLKVVGAR ENNLQGIDVK IPLGVLCCIT GVSGSGKSTL VNQILAKVLA
NKLNRARQVP GRAKRVEGLE HLDKLVQVDQ SPIGRTPRSN PATYTGVFDK VRNLFAETTE
AKVRGYKPGR FSFNIKGGRC EACQGDGTLK IEMNFLPDVY VPCEVCDGQR YNRETLEVKY
KGKNIAEVLG MPISEAADFF EPITSIHRYL ATLVDVGLGY VRLGQAATTL SGGEAQRVKL
AAELQKRSNG RTVYILDEPT TGLHFEDIRK LMMVIEGLVD KGNSVIIIEH NLDVIKAADW
IVDMGPEGGS GGGTVVAEGT PEQVAEVAGS YTGQFLKELL

> RXA02418 (1-567, translated) 189 residues
VVRYVKFSRT ANRGVHISAE ARINERIRVP EVRLVGPNGE QVGIVRIEDA RKLAFDADLD
LVEVAPNAKP PVCKIMDYGK FKYEAAQKAR ESRKNQQQTV VKEQKLRPKI DDHDYETKKN
NVIRFLEKGS KVKVTIMFRG REQARPELGY RLLERLANDV VDFGIVETRA KQDGRNMTMV
LGPVRKGKK

> RXA02429 (1-2289, translated) 763 residues
VAGFDWFWKA LGGKSGRNQK RSVAIVNQVE NHAAELDALD DVALAQRAKD LASGGRIDNH
AEFLAILGVA SQRTLGLKPY PVQSQAVLRL IEGDVVHMAT GEGKTLVGAM AATGLGLMGK
RVHSITVNDY LAVRDAEWMR PLVEFFGLSV ASISEKMDAG ERRQAYKAAI VYGPVNEIGF
DVLRDQLITR REDAVQHGAD VAIIDEADSV LVDEALVPLV LAGNQPGHAP RGKITDVVRS
LKENDDYTID DDRRNVFLTD KGAAKLEQQL GISSLYDDEH VGSTLVQVNL ALHAQALLIR
DIHYIVRDSK VLLIDASRGR VADLQRWPDG LQAAVEAKEG LAVSEGGKIL DTITLQALIG
RYPMACGMTG TAVEATDQLR TFYDLHVSVI ERNHPLKRFD EADRIYATMA EKNRAIIDEI
ALLHSTGQPV LVGTHDVAES EELATALREL NIEVSVLNAK NDAEEAQIIA EAGDIGRVTV
STQMAGRGTD IRLGGADEAD YDEVVKLGGL AVIGTARHRS QRLDNQLRGR AGRQGDPGLS
LFFVSLDDDV VVSGGSRESV SAQPDATGLI DSDRIRDWVG HCQRVTEGQL LEIHSQSWNY
NKLLADQRVI IDERRERLLD TALAWEELAQ HAPARAAELE DLDQSVREQA ARDIMLYHLD
YNWSEHLALM DDVRESIHLR AIARETPLDE YHRIAVREFK DLAQRAVDDA VSTFKSVTID
HEGAHLDDEG LARPSATWTY MVSDNPLAGS GNSVISGIGN IFR

> RXA02436 (1-561, translated) 187 residues
VVGISLDVVM MGVMTSKTAT AILHTNRGDI TIDLFGNHAP ETVANFVGLA QGTKDYQSAN
AQGDSEGPFY NGSVFHRVID GFMIQGEDPT GTGRGGPGYT FADEFHPELR FDRAYLLAMA
NAGPGTNGSQ FFITVTPTPH LNNAHTIFGE VTDAESQKVV DAIATTATDR YDRPADAVVI
ESVEITA

> RXA02445 (1-1689, translated) 563 residues
VEPFELEKDL ERLRKNGKDD ETVEVKSWGR LPLSKGSKSF WESLSAFANT NGGYILLGLS
EPDFTPVEGF DSQASIQFIR AGLNPQDRDA QKVEPVPHHE IHEMTVDGAE VVLVSVSPLS

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VNGPCYYLPV  GITNGSFKRV  GDEDRKLSHL  EIYELQNRFV  QTKTDRNPVP  DSSIDDLNNQ
LAASFKQRLI  ESNSRSLGTD  DNWLLRKNIT  TSKGELTIAG  LLALGSYPQQ  FFPRVIIDVA
VHPGLHKSPI  GTSIRFEDRK  ICEGNLLEMV  QEAMSAIKRN  LRVRRVVEGL  SGKDVLEIPE
EVLREALANA  VLHRDYSELA  QNEAIHVDIY  KDRVEITSPG  GLPNGKRPES  ILDGYSEPRN
RVLSRILMDI  PWTHEVQGVL  AESNGTGVPR  MFNLMREAGL  PVPNFKIDIS  SVTVELSRHG
LLDAQTSEWL  VEKLGSDFSN  TQGIALVLAK  ELGAVTSRDL  RNQTGHDSED  MRSLLDALVD
RGVLNQNLQN  QYQLATSSVN  VTQSEQEVLD  AINKTTPVTI  REIATKTGKT  ASSLRPLLRG
LVEAGLVVAT  APPSSRNRAY  LKA
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> RXA02456  (1-618, translated) 206 residues
MAENRTGTVD  GDALAARFEE  EALPLLDQLY  GGALRMTRNP  ADAEDLVQDT  YIKAYQAFAS
FKPGTNLKAW  LYRIMTNTYI  NMYRKKQRQP  SQTSADEITD  YQLVESQSHT  STGLESAEVE
ALKNLPDGKI  GDAMNQLSPE  YRMVVYYADV  EDLAYKEIAE  IMDVPLGTVM  SRLHRGRKQL
RGMLKEVAKE  QGIGLEHPDM  KKNSEA
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> RXA02462  (1-915, translated) 305 residues
EAGGLYVLGT  ERHESRRIDN  QLRGRSARQG  DPGSTRFYLS  MRDDLMVRFV  GPTMENMMNR
LNVPDDVPIE  SKTVTNSIKG  AQAQVENQNF  EMRKNVLKYD  EVMNEQRKVI  YSERREILES
ADISRYIQNM  IEETVSAYVD  GATANGYVED  WDLDKLWNAL  EALYDPSINW  TDLVEGSEYG
KPGELSAEDL  RTALVNDAHA  EYAKLEEAVS  AIGGEAQIRN  IERMVLMPVI  DTKWREHLYE
MDYLKEGIGL  RAMAQRDPLV  EYQKEGGDMF  NGMKDGIKEE  TVRQLFLSAS  SSSSKTRKSL
TNSEP
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> RXA02476  (1-879, translated) 293 residues
MSFTAFQTAL  LVWFRANARD  LAWRDPNTSA  WGILLSEVMS  QQTPVARVEP  IWREWMEKWP
TPEDFANAST  DEILRSWGKL  GYPRRALRLK  ECAEVIVEKH  AGEVPDTVEA  LLALPGIGDY
TARAVAAFHF  GQRVPVVDTN  VRRVYQRAVA  GRYLAGPAKK  QELIDVSLLL  PNTHAPEFSA
AIMELGALIC  TATSPKCDTC  PLLDQCQWQK  LGCPSPSEEE  LASAKKRVQK  FVGTDRQVRG
LIMDVLRNAT  APVPLSAIDV  VWPDDAQRSR  ALFSLIEDGL  AEQNEAGYFH  LPR
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> RXA02502  (1-1392, translated) 464 residues
MVSVLIVGMS  HRSAPVSLLE  RLSMDDSVRG  ETTQALLGRA  SLSEALIVST  CNRLEVYTVT
SSFHTGVNDV  VEVLHEASGV  DIETLRGYLY  VRYADAAAEH  MLVVTSGLDS  MVLGEQQIIG
QVRTAYQAAN  EYGSVGPALH  SLTQTALHTG  KRVHSETAID  DAGASMVSFA  VDRALVQMGL
DSEAEAPLSG  KTALVLGAGA  MSSLAATHLG  RAGISNLIMA  NRTLERAERL  AEHSLEAGVP
AEVVEYDQRA  SAYNRVDLVV  SATGADDFTV  KPEDIPEGAS  LMLVDLSMPR  DIDDACADLP
GVDLVNIERL  HKASREGGSG  MAPSEEEALA  IVREELDSFT  SEQRIRDIVP  AVSALRRQAA
SVGSDELDRL  RQRAPGISEV  EWGEVEKTGR  RVVDKLLHEP  TVRVKELAAR  SGSISYDSAL
QELFGLESLA  STAAPATTSV  NASELPDAGI  VAFVNAPSAT  QTRE
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> RXA02509  (1-1971, translated) 657 residues
DLPNKGPEAI  VCAKDAEGQL  KDLSHVPETT  ATFTAVPANT  DDGRAVIRHS  CAHVLAQAVQ
AEFPGTKLGI  GPAIENGFYY  DFDAAEPFTP  EDLKTIEKRM  KKIIKTGQKF  ERRVYESAEA
AAEELKNEPY  KLELIQDKGN  VDPNSDEATE  VGAGELTAYD  NVNPRTSEVE  WSDLCRGPHI
PTTRYIPAFA  LTRSSAAYWR  GDQDNAGLQR  IYGTAWEDKE  SLDAYQTMLA  EAEKRDHRRL
GTELDLFSFP  DDLGSGLPVF  HPNGGIVRNE  MEDHSRRRHI  AAGYSFVNTP  HITKQDLFER
SGHLGFYKDG  MFPPMQVDAE  FDEDGNVTKP  GQEYYLKPMN  CPMHNLIFDS  RGRSYRELPL
RLFEFGNVYR  YEKSGVIHGL  TRARGFTQDD  AHIYCTEDQL  EAELTSVLDF  ILSLLRDYGL
DDFYLELSTR  DPKKSVGSDE  IWERSTEILN  RVATNSGLEL  VPDPEGAAFY  GPKISVQARD
AIGRTWQMST  VQLDFNMPER  FNLEYTSSDG  SKQQPIMIHR  ALFGSIERFF  GVLLEHYAGA
FPAWLAPHQV  MGIPVADDCI  PHLETITAQL  REKGIRADVD  TSDDRMQKKI  RNHTTGKVPF
MLLAGARDVE  ANAVSFRFLD  GTQVNGVPVD  EAIAVISSWI  GDRINDQPSE  DSIAARR
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```
> RXA02523  (1-819, translated) 273 residues
VTIFPEYLDP  LRHALLGKAI  EDGILEVGVH  DLRNWATGGH  KAVDDTPYGG  GPGMVMKPEV
WGPALDDVAA  GRVSGAELDS  ASLHLKNVRH  DELGGVEKRA  YVVEEDRDLP  LLLLVPTPAGK
PFTQADAQAW  SNEEHIVFAC  GRYEGIDQRV  IDDAANRYRV  REVSIGDYVL  IGGEVAVLVI
AEAVVRLIPG  VLGNRRSHEE  DSFSDGLLEG  PSYTKPRTWR  GLDVPEVLFS  GNHAKVDRWR
RDQALLRTQA  IRPELIDASL  LDSTDLKVLG  LDK
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> RXA02557  (1-588, translated) 196 residues
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MSSLIVGTDG LSRPSWAAQD PLMRDYYDTE WGMPIRDEQG LFERVSLEAF QSGLSWATIL
RKRDSFRAAF SQFDPELVAK FTDADIERLM EDAGIVRNKR KILATINNAK ATLQLREKGG
LVEFVWGFKP IDTPQPETLE EIPTQSPESV ALSKALKKEG FSFVGPTTMF ALMEAIGIVD
THLVGSHRRG SSGVWA


> RXA02563 (1-732, translated) 244 residues
MMPYITDIAA LEHVGVAAAW TEKVPAFRVL REKRMLDFRA PITVITGENG VGKSTLLEAI
AINAGFDTAG GEHTGKFKPS DNPLQTVAKA HKGKEPMRGY FLRAETHFNV ASGYRDEAPG
WVNLHHMSHG ESVMHIVQNA FVGKGLYLMD EPEAGLSFIR QMAILAELNF LAESGAQIII
VTHSPVLMAI PGAEIWEFSA SGELHRGFDF EVTTAFRALR DFFEDPEEIA EYMMDVMMDN
KGES


> RXA02590 (1-936, translated) 312 residues
MGISLLSSLL KIHGFPVVAD FFFALAVVVA IVIIGGWLIY RSPSFKTEVM PAWAMLSMGL
IALGTASPVV LGDDLWGFMF VCWSIGTAVG LVAYSLYITA ILRSKAGTPT FAWGLPLVTP
MVASTSAAQL HEHFELPAML WVSFGLFLLT LASAPAVFTR VYFYYFGPKA QGIPLMATPT
SWIPLGMVGQ STAAAQLIGA SFGSKTAITM GIIYGIIMGI FTIPLGAIAH FVFYRAVFKG
ATYSPTWWAS TFPVGTLSLG AHFLSQSTGV EWFNYFSLYL IALMLFHVIV STIAGTIAVM
RRIVGKLKSQ LA


> RXA02607 (1-219, translated) 73 residues
MRDTAFRSIK AKAQAKRRSL WIAAGAVPTA IALTMSLAPM ASAQSSNLSS DAVIGSIAQG
VTDGLTDYLK PRV


> RXA02608 (1-1695, translated) 565 residues
VRVISAEWAT SKHVILTIQS AAMPERPIKV QLLLPRDWYS SPNREFPEIW ALDGLRAIEE
QSGWTIETNI EQYYADKNAI VVLPVGGESS FYSDWEGPNN GKNYQWETFL TQELAPILDK
GFRSNTDRAI TGISMGGTAA VNIATHHPDM FKFVGSFSGY LDTTSAGMPI AISAALADAG
GYDANAMWGP VGSERWQEND PKSNVDKLKG KTIYVSSGNG ADDFGKEGSV AIGPANAAGV
GLEVISRMTS QTFVDRASQA GVEVVASFRP SGVHSWEYWQ FEMTQAFPHI ANALGMSTED
RGVECAPVGA IADAVADGAM GTCLTNEYDV TGGKAQDFAN GRAYWSANTG AFGLVGRINA
RYSELGGPAS WLGYPTSSEL KTPDGRGRFV TFEHGSIYWT ATTGPWEIPG DMLAAWGTQD
YEKGSLGYPT GAAVEYNGGL RQQFEGGYVF RTSNNQSYWV RGEISKKYAE DGIFAQLGFP
TGNEKLINGG AFQEFEKGNI YWSASTGAHV ILHGDIFDAW GAKGWEQGEY GFPTSDQTAI
TAGGQTIDFQ NGTIRQVNGR IEESR


> RXA02625 (1-786, translated) 262 residues
MTAAFYDLMD FDEVLEKYDP VMGLEVHVEL GTETKMFSAS SAHFGAEPNS NVDPVSLGLP
GALPVVNAKG VEWAIKIGLA LNCSIAESSR FARKNYFYPD QPKNYQISQY DEPIAYDGYL
DVVLEDGTEW RVEIERAHME EDTGKLTHLG GTSGRIHGAT ASLVDCNRAG VPLIEVVTKP
IEGAGARAPE IAKAYVSALR DLVKALGVSD GRLDQGSMRV DANLSLRPIG QEEFGTRTET
KNINSLKSVE QASTFEMQRQ AQ


> RXA02671 (1-579, translated) 193 residues
MKSGCFEQQS DGIKEVPDPS GLFLSHRGST PDGTAVTVAM DGVRPLLAEV QSLLVDAPSK
NPRRVVTGLD ANRVPMVLAV LSARAGRQTQ GKDAYVATVG GMKVGEPATD LAVALATASA
LAKKPLPDKT VVLGEVGLAG EIRRVPNVDR RLAEAERLGY EKAVIPGGSG IKQTSLRVIE
ASTLAEALAA VSL


> RXA02686 (1-1137, translated) 379 residues
MSVAQLANRL AQLSPAEHGF AWFDPEITAG HGVGPLHGMV IPAKDLNDVA GMPTAFGNAS
RRKVATDTDP FIQNLIDRGA IIAGKTQTSE LGMTAYCEPI DMDAPSNPVL PGHTPGGSSG
GAAVAVARSL VDAAHASDGG GSIRVPAAAC GLVGFKPAHD SSGGNPSTQG FITRDVATQV
RLHALQPRTR RLRIGVLAEP IHANSLVDAP FLSILESTAH LLEKAGHEIV SVPLPYGAWA
FDAYTEVFMM KSAGLTNLGS PITRWLSEQG RSLSPSDRQS SVKAFDSVAE TVHGAWDIDV
LLTPTLAYAP PKIGYFSSMP PEEDFLAQTK WTPWATLFNM TGGAAISVPV EGVGIHLGGI
RVRDEDLLGL AAFVERAVA


> RXA02692 (1-1266, translated) 422 residues
MIDLKFLRDN PDVVRASQIT RGEDPALVDE LISADESRRE AIKAADDLRA EQKAFGKKIG
QASPEDRPAL LEGSNELKAK VKDAEAAQEA AEAKVNELQM KLSNVVSGAP AGGEDDFVVL
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ETIGEPRTFD FEPKDHLELG ESLGLIDMKR GTKVSGARFY YLTGDGAMLQ LGMLMLAAQK
AREAGFSMMI PPVLVRPEIM AGTGFLGDHS EEIYYLERDD MYLVGTSEVA LAGYHKDEII
DLNEGPVKYA GWSSCFRREA GSYGKDTRGI LRVHQFDKVE MFVYCKPEDA EDVHQQLLGM
EKEMLAAIEV PYRVIDVAGG DLGASAARKF DTEAWVPTQD TYRELTSTSN CTTFQARRLQ
TRYRDENGKP QIAATLNGTL ATTRWLVAIL ENNQQADGSV VVPEALRPFV GKDVLKPVKQ
AG
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> RXA02726 (1-2934, translated) 978 residues
```
LFLATRPCRG YRVPRVFSWD THGLPAELEA EKQLGIKDKG EIEAMGLAKF NEYCATSVLQ
YTKEWEEYVT RQARWVDFEN GYKTMDLSFM ESVIWAFKEL YDKGLIYQGF RVLPYSWAEH
TPLSNQETRL DDSYKLRQDP TLTVTFPVTG VVEGSSANAG LVGALALAWT TTPWTLPSNL
ALAVNPAVTY ALVEVAEDGE AEFVGKRVLL AKDLVGSYAK ELGAEAVIVS EHPGSELVGL
TYEPIFGYFR DHANGFQILG AEYVTTEDGT GIVHQAPAFG EDDMNTCNAA GIEPVIPVDI
DGKFTGLVPE YQGQLVFDAN KDIIKDLKAA GRVVRHQTIE HSYPHSWRSG EPLIYMALPS
WFVNVTEIRD RMVEVNQDIE WMPAHIRDGQ FGKWLEGARD WNISRSRYWG SPIPAWVSDN
DEYPRVDVYG SLDELEADFG VRPKSLHRPD IDELTRPNPD DPTGKSTMRR VTDVLDVWFD
SGSMPFAQVH YPFENKEWFD THAPADFIVE YIGQTRGWFY LLHVLSTALF DRPAFKKVVA
HGIVLGDDGL KMSKSKGNYP NVNEVFDRDG SDAMRWFLMS SPILRGGNLI VTEKGIREGV
RQAQLPMWNA YSFLQLYTSK NATWSVDSTD VLDRYILAKL HDLVAETQAA LDGTDIAKAC
DLVRNFCDAL TNWYVRRSRD RFWAGDEAHP EAFNTLYTVL ETLTRVAAPL LPMTTEVIWR
GLTGERSVHL TDFPSAESFP ADADLVRTMD EIRGVCSAAS SVRKAHKLRN RLPLPGLTVA
LPDSARLADF ASIIRDEVNV KNVDLTSDVD SVGTFEVVVN AKVAGPRLGK DVQRVIKAVK
AGNYTREGDV VVADGIELNE GEFTERLVAA NPDSTAQIDG VDGLVVLDME VTEELEAEGW
AADAIRGLQD ARKNSGFEVS DRISVVVSVP EDKKEWITTH ADHIAAEVLA TSFEIVTDAL
DGETHDIVAG VTAKVTKN
```

> RXA02731 (1-2097, translated) 699 residues
```
MAFAAEHPVL SHSEHRPVGE IERSDDKFVV VSEFEPAGDQ PAAIKELDER LDRGERDVVL
MGATGTGKSA TAAWLIEKQQ RPALVMAPNK TLAAQLANEL RQLLPNNAVE YFVSYYDYYQ
PEAYIAQTDT YIEKDSSINE DVERLRHSAT SSLLSRRDVV VVSSVSCIYG LGTPQSYLDR
SVVLNVGEEI DRDRFLRLLV DIQYERNDVG FTRGAFRVKG DTVDIIPAYE ELAVRIEFFG
DEIDALYYIH PLTGDTIRQV NEIRIFPATH YVAGPERMEK AVADIKAELE VRLADLENRG
KLLEAQRLRM RTEYDLEMIE QVGFCSGIEN YSRHIDGRGE GTAPATLIDY FPEDFLTIID
ESHVTVPQIG GMFEGDMSRK RNLVEFGFRL PSAMDNRPLT WEEFDERRGQ TVFMSATPGK
FEIAAADGEF VEQVIRPTGL VDPKVTVKPT KGQIDDLIHE IRQRTDKDER VLVTTLTKKM
AEDLTDYLLE NGIRVRYLHS DIDTLQRVEL LRQLRLGEYD VLVGINLLRE GLDLPEVSLV
AILDADKEGF LRSTTSLIQT IGRAARNVSG EVIMYADKIT DSMQYAIEET DRRREKQVAY
NKEHGIDPQP LRKKIADILD QVYDNSADGA GPSASGDAAV VAKPDVSSMP AKEVQKLIDD
LSAQMAAAAR ELKFELAGRL RDEIFELKKE LRGIKDAGI
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> RXA02742 (1-2349, translated) 783 residues
```
MSEQRLDQLE RRLSELEREI AAIRQEIRQE RLVLPEPEPV KVDTVIATEA TGVNASSGPE
AKIALFMERF SGRHDVYARR WTSRKTGKSG WSPATRQGFY SKDTTPKDYL PFTVDTVNAH
LRRGGDHIGL YVMVPIDTCK LLACDFDDGT WKQDAAAFVS ACTDHGIDAL AEISRSDDGA
PVWIFFDTPI SAMLARRLGF AMLRQAMNSR PDMDMSSYDR FFPAQDTIAT RANGSARLGN
LIALPLNGDC RARNTAVFAD SETWVPFEDP FAALAAITPL ATEKIEQILA TTQEKFGPEP
EHIKRPTRAE LKQVKANGET IKLTITNELS VPTERLPAAV IAEIKHRAVI PNPEFYRRQA
QRFSTFGVPR IVIRFAQAEQ RLLLPRGLVD DTLRILTLAG YKVSVIWPRQ TRKTIDASFE
GELRSMQQEG IDSLKGQRTG VLVAPPGAGK TVMACALIAN RKIPTAVIVN RAELISQWRD
RLAQYLSIDA DSIGQIGAGR RKTTGIIDLI TVQSLSRKDS DPKILEQYGQ IIVDECHNIA
APGAEAALNQ VKAPYWLGLT ATPFRSDHMD EIITMQCGPV RHRMEVATDN EQRLIHIHET
SFDSEETTEI QDLYNELAVD SARNAQITAE VHKALEAGDR CLVLVNRIAA LEALTSSITE
SGDHTVLVMH GRQTQEERVH LRAQLASLSE KQDPFVLVAM NKVAGEGLDI PSLNTLFLAA
PVSFKGLVIQ QIGRVTRATG DQNAPPVTAT VHDFVDSKIP TLKRMHGRRL RAMQKEGFAV
SEP
```

> RXA02748 (1-1641, translated) 547 residues
```
VFESLSDRLN SALSGLRGKG KLTEADINAT TREIRLALLE ADVSLTVVRA FINRIKERAA
GAEVSQALNP AQQVIKIVNE ELVQILGGET RRLSLAKNPP TVIMLAGLQG AGKTTLAGKL
SKHLVKQGHT PMLVACDLQR PGAVQQLQIV GERAGVTTFA PDPGTSIDSL EHEMGTSHGD
PVEVARAGIE EAKRTQHDIV IVDTAGRLGI DETLMTQARN IREAINPDEV LFVIDSMIGQ
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DAVDTAEAFR DGVDFTGVVL TKLDGDARGG AALSIREVTG KPIMFASTGE KLDDFDVFHP
ERMASRILGM GDVLSLIEQA EAVMDQEKAE VAAQKLGSGE LTLEDFLDQM LMIRRMGPIG
NILKMLPGGK QMSQMADMVD EKQLDRIQAI IRGMTPAERD NPKILNASRR KRIANGSGVT
VSEVNKLVER FFEARKMMGQ MAGQFGMGPG SRSATKKQAK GRKGKNGKRK PAKKGPTQPK
MPMGGMPGMP GMPGMGGAGM PDLAELQKQL GGAGGGMGGL GGGLPGMPKP PKGMENIDLN
NLDFGKK
```

> RXA02788 (1-2664, translated) 888 residues

```
VQTHEIRERF TNHFVNAGHQ AVPSASLILD DPNLLFVNAG MVPFKPYFLG QQTPPFENGT
ATSIQKCVRT LDIEEVGITT RHNTFFQMAG NFSFGQYFKE GAITHAWGLL TGSVADGGFG
LDPERLWVTV YLDDDEAAEI WEKKIGVPSE RIQRLGMADN YWSMGVPGPC GPCSEIYYDR
GEKYGKEGGP VADDNRYMEI WNLVFMEKER GQGIGKDNFD ILGDLPKKNI DTGMGVERVA
CILQDVENVY ETDLLRPVID VAETLTGTKY GSDNTSDIRF RVIADHSRTG MMLILDGVTP
GNEGRGYILR RLLRRIIRSA RLLGATGETM EQFMNTIMDT MTPSYPEIAD NRERIMRVAV
TEERAFLKTL VSGTHLFEEA ATSIKAAGST KVAGAQAFAL HDTYGFPIDL TLEMAAEAGL
EVDVEGFDSL MAEQRSRAKA DSQAKKHGHT DLSIYREWVD NNPTVFTGFE ELDSQSKVLG
LLSDGAKISE ATEGQEVEVI LDQSPLYAES GGQLGDRGQI LLGDTVLDVH DVQKIGKKLW
VHKALVANGG LAVGDEVVAS VDKQWRHAAR QAHTATHLIH AALRQVLGPT ALQAGSMNKP
GYLRFDFNYT EQLTPAQVEQ IQAITNEAVD TDWAVNTVET SLEEAKAMGA MALFGENYGS
TVRVVEIGGP FSMELCGGTH VAHSSQIGPV ALLGESSIGS GVRRIEAYSG LNSFNYLSKE
RALAEGLASS LKAPSEELPE RVAQLVDKLK AAEKEIEALH RQQLMAQTAD LLNNAQEIGG
VTTLLLRVKD NTNAGDLRTI ATTLKDKLGD REGVLVIASD NAGKVPFVVA ATKAAVARGA
HSGNLVKLVG SYIDGRGGGK ADLAQGSGAN IAGLESAFGA VRAEIEAL
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> RXA02822 (1-570, translated) 190 residues

```
GTEVSHPAHG AWSQFKFEGG VHRVQRVPVT ESQGRIQTSA AGVLVYPEPD EVENVEIDEK
DIRVDVYRSS GKGGQGVNTT DSAVRITHLP TGLVVTCQKE RSQIQNRARA MQVLAARLQA
MKEEEAAAEA ATGRAAQIRT MDRSERIRTY NWPENRISDH RIGFKANNLD SVLDGELDDL
FTALQAAERA
```

> RXA02837 (1-174, translated) 58 residues

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MNTKLHAVTD ATGRPIRFFM TAGKVSDYIG AMALLGSLPK AGWLLADRGY DADWFRDA
```

RXA02860 (1-438, translated) 146 residues

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DLQNPTAKMS KSGDNPKGII NLLDDPKVST KRIKSAVTDN DGVIAYDPEN KPGVSNLLVI
QSALTGTSID SLVDGYQGAG YGALKGDTAD ALEAFTTPLK AKYDEYMNDR GELERVLAIG
AERATEVANE TLADVYDKIG FLASRR
```

> RXA02866 (1-480, translated) 160 residues

```
MTTQDKDLTA QTASRVLSGI QPTADSYHLG NYLGAVKQWI DLQDSYDAFY FIPDLHAITV
DQEPEELRNR TISGAAQLLA LGIDPERSTL FVQSHVPAHA ELSWVLTCLT GFGEASRMTQ
FKDKSSKRGA DRTSAGLFTY PMLMAADILL YRPHLVPVGE
```

> RXA02886 (1-831, translated) 277 residues

```
MKLFSKAAGV IAAALLVAGG IAPVAGGQAS QVVTPEDQDA YVQQFHHEGN TPPVVDGVGG
YTEQEIAEIH EAIRQAQESG APNEELIPGE MWSDKVELPV TIDKAAADEA EIAIAQQQSQ
PQTRGLAAAA ACQTFWPSPH QVCGAILERY IQQGAQFGWM LFPSEGQTLN PDGQGYRQRF
MNGFVYWHPT TGAHAVNNYS AQVWERNGWE SGWMGYPTGG EVPVNGSNPI DGELSGWVQT
FQGGRVYRSP VLDGFQVASI NGLILDKWLE LGGPDSD
```

> RXA02890 (1-1083, translated) 361 residues

```
MHEGRRYSAP HTFGTKGEAQ EFLASERTAI INGTWMDFEM RERFEQAQRE AEERMMETFF
SYASRWIETR TNAQGKKLSQ GVKDDYFRYI KSDRLSYWAD YALCEITVAD VREWYSDTIQ
DGKLTSMARS YSMMKSVMET AVEDGIIPMN PCKVRGGGNT KTGKKVDVPT DAELEAIIGA
LPSKYFCLAI VAAAGALRFG EIVALRTTDV DVYFDRSGFV DCVRIRISRS IRHTRYHGRV
EGPPKTEAGV RSLYIYGKDA AEIAKHVDTI DVGLRLWSSM RDPDEPMPYH TFKHNWDRAR
ESVHSKATVH SMRHYSGTKY AQVGATLKEV MARLGHSTPS AALRYQHSGE RDEELAKRMA
R
```

> RXA02894 (1-786, translated) 262 residues

```
FLMHELPEPL EAAIGADGQR SIVGMSMSGG SVLNFATHDP NFYSSVGSFS GCAETNSWMG
```

```
RRGIAATAYN GNVVPEQIFG EVDSDYSRYN DPLLNAAKLE EQDNLYIFAG SGVFSELDVI
GDNAPIDEDA FKNRVLVGFE IEAMSNTCTH NLKAATDQMG IDNINYDFRP TGTHAWDYWN
EALHRFFPLM MQGFGLDGGP IPVYNPNGVS SSESSSELSS DVSLGTVIGS VAGSSGSSEG
SSVREFLAGS SGSSQSTGSF YE
```

```
> RXA02904  (1-675, translated) 225 residues
TDPRYPLGKD DLPKATIDME PEALARLERF VGVDGDRIRQ INAYSPSMGR TIPLVWVVPE
DNTVPGPTVY ALGGGDGGQG GQNWVTRTDL DELTSENNIN LIMPMLGSFS FYADWAGESE
SMGGAQQWET FLMHELPEPL EAAIGADGQR SIVGMSMSGG SVLNFATHDP NFYSSVGSFS
GCAETNSWMG RRGIAATAYN GNVVPEQIFG EVDSDYSRYN DPSIL
```

```
>RXN00046 TRANSLATE of: rxn00046.seq check: 4489 from: 1 to:  696
MDLNTQRSKLYAQLQGQLIVSVQAPDGHAMRDTHTLTHVAAACVDGGAPAIRCGGYGGLE
DIRSISNRVDVPVFGLTKEGSEGVYITPTRDSVRAVAESGATVVCADATFRPRPDGSTFA
ELVTVAHDSGILIMADCATPEEVLSAHKAGADFVSTTLAGYTEHREKTVGPDFDCLREAR
ELVPDAFLIGEGRFSNPADVAHGRLIGANAIIVGTAITDPGFITGQFASLLH
```

```
>RXN00083 TRANSLATE of: rxn00083.seq check: 5101 from: 1 to:  300
VLALPSSIIDPLWCQFAALIPPVTDTHPLRCHRPRIPDRIIFDKLIQVLVLGASYAKIAD
TTCSATTLRTRRDEWITAGIFEQLEQICLEFYDRIVGLDL
```

```
>RXN00127 TRANSLATE of: rxn00127.seq check: 8871 from: 1 to:  465
VWTLSPYDGPHRNVLIALKEHGRADLVAFVGAVVGASISYLAAQGEIEHDITLVPAPTRA
TSRRRRGGDPVERVCNASRLSTFPCLQISSRTPDSVGQTAQQRRLNMRVELVRQPRGSVL
IIDDVVTTGATISASANVLRAAGVQVRGALTYCQA
```

```
>RXN00172 TRANSLATE of: rxn00172.seq check: 1609 from: 1 to:  612
MFGSSFKEQTTNPRSQRVSYLRVSSTDQNLARQREAVNHSGHIDREFTDELSGGAKSHRP
GLEDCINYLREDDVLVVASIDRLARSLVDLRVIIDRITDKGASVIFLKENLTFAAGRDDP
RANLMLGILGSFAEFERSIIRERQAEGIALAKKAGKYAGRPKALDKEQIQEAKDMIAQGE
TKSAVAKHFGINRSTLYEYLKNPD
```

```
>RXN00211 TRANSLATE of: rxn00211.seq check: 7693 from: 1 to:  663
MSFLIRVLLSDTPGSLALLAEALGIVEANIQSVDVVERFPNGTVMDDLVISIPRDVMADT
IITAAEEVDGVEIDSIRPFSGTVDRRGQIQMLAAVAHQRRDITAAMEEMVDVIPRTMTSG
WALVIDLKGPITRIAGSLAAPEDDGTVPENIVLKEARMLNPENDPWIPESWTLLDSSLAI
APIGKHGLALIIGRPGGPDFLASEVEHLGQVGDIIGAMLQK
```

```
>RXN00380 TRANSLATE of: rxn00380.seq check: 9027 from: 1 to:  621
VRLTKLAATIGCVTLSGLALVACSSDSTAGTDAVAVGGTFQFHSPDGKMEIFYDEADRQQ
LPDIGGDSLMEEGTQINLSDFENQVVILNAWGQWCAPCRSESDDLQIIHEELQAAGNGDT
PGGTVLGINVRDYSRDIAQDFVTDNGLDYPSIYDPPFMTAASLGGVPASVIPTTIVLDKQ
HRPAAVFLREVTSKDVLDVALPLVDEA
```

```
>RXN00454 TRANSLATE of: rxn00454.seq check: 9628 from: 1 to: 1293
MGGEAGCTLDLAPMSDLSFTLNNKLADDAPGKHGRTGVIHTPHGDIATPAFIPVATKATV
KTLTPEQIRETGAQAILSNAYHLYLQPGPDIVDEAGGVSAFENWHGPTYTDSGGFQVMSL
GSGFKKVLAMDTTNLTRNDIKAAKKERMALVDEDGVDFKSVIDGSKHRFTPEVSMQIQHQ
LGADIIFAFDELTTLVDTYDYQVESVERTRRWAQRCLLEHERLTQERVDKPLQSLWGVVQ
GAQFEDLRRQAVKGLLDLDRQAADEGRRGFGGFGIGGALEKENLGTIVGWVCDELPEDKP
RHLLGISEPDDLFVAVEAGADTFDCVAPTRLGRRGGVYTLDGRMNLTGARFKRDFKGIDE
EVGGYASENYSRAYIHHLLKAKEFLAGTLCTMHNLHFMITLVDKIRASIDDGTYYEFKEE
FLGRYYASKVS
```

```
>RXN00458 TRANSLATE of: rxn00458.seq check: 4019 from: 1 to:  636
MAGRYAPSPSGDLHFGNLRTALLAWLFARSEGKKFLMRVEDIDEQRSSKESAESQLADLS
ALGLDWDGDVLYQSTRYDAYRAALEKLDTYECYCSRRDIQEASRAPHVAPGVYPGTCRGL
KEEERVEKRATLAAQNRHPAIRLRAQVTSFDFHDRLRGPQTGPVDDFILLRGGQEPGWAY
NLTVVVDDAYQGVDQVVRGDDLLEFGARQATL
```

```
>RXN00484 TRANSLATE of: rxn00484.seq check: 6349 from: 1 to: 1080
```

VDATLKKNLRDKGIEVHSHPGFLLTEPWEVSTATGTPYKVFTPFSKAAWEVARVHAYETV
KNNVPVPSHLTGPEDVELPILEMEQPFWSTTLVKECAPGEKNASEKLFDFLEHLQDYPQA
RDSLARSATSKLSAHLRFGEISIHRVWAETAAIDSEGTELFLKELLWRDFAWHRLYALPH
MDTQNVRMQFNRFGWSWDPSEKDKLNTPSTPLIPTKADQFHEDLAAWRAGKTGIPLVDAG
MRELWATGSMHNRVRMVVASFLTKNLQIHWRHGEEWFWETLVDADPASNAFNWQWAAGSG
DDASPYFRIFNPVTQAKKFDPDETYIRRWVPEYGTPSYPDPIVDLKESRQIALDAYSAIK

>RXN00493 TRANSLATE of: rxn00493.seq check: 4601 from: 1 to: 1614
MAKLIAFDQDAREGILRGVDALANAVKVTLGPRGRNVVLDKAFGGPLVTNDGVTIARDID
LEDPFENLGAQLVKSVAVKTNDIAGDGTTTATLLAQALIAEGLRNVAAGANPMELNKGIS
AAAEKTLEELKARATEVSDTKEIANVATVSSRDEVVGEIVAAAMEKVGKDGVVTVEESQS
IETALEVTEGISFDKGYLSPYFINDNDTQQAVLDNPAVLLVRNKISSLPDFLPLLEKVVE
SNRPLLIIAEDVEGEPLQTLVVNSIRKTIKVVAVKSPYFGDRRKAFMDDLAIVTKATVVD
PEVGINLNEAGEEVFGTARRITVSKDETIIVDGAGSAEDVEARRGQIRREIANTDSTWDR
EKAEERLAKLSGGIAVIRVGAATETEVNDRKLRVEDAINAARAAAQEGVIAGGGSALVQI
AETLKAYAEEFEGDQKVGVRALATALGKPAYWIASNAGLDGSVVVARTAALPNGEGFNAA
TLEYGNLINDGVIDPVKVTHSAVVNATSVARMVLTTEASVVEKPAEEAADAHAGHHHH

>RXN00669 TRANSLATE of: rxn00669.seq check: 6043 from: 1 to: 882
MDNSTVRIRLDLAYDGTDFHGWAKQGTSDLRTVQKVLEDNLSMVLRETVELTVAGRTDAG
VHAAGQVAHFDIPAHALEQRSIDGDPSKLVRRLGRLLPDDIRVHGVRFAEPGFDARFSAM
RRHYVYRITTHPAGALPTRRHDTAQWPKPVELERMQLAADALLGLHDFVAFCKAKPHATT
VRELQKFAWKDVSTDIEPQVYEAHVVADAFCWSMVRSLVGSCMAVGEGRRGSGFTAELLD
ASERSPMVPVAPAKGLSLVGVDYPSADKLQERALETRAVREFPDASASLKLDDE

>RXN00737 TRANSLATE of: rxn00737.seq check: 824 from: 1 to: 993
MKVSDIRQFSVADQRTIPEITIKSIEIFPARELLITEEVASRAESLISKHPGNPTLVEML
SRIADSQDVDGMEALIPALTDTPMVPMLELMPENTHVLVIAPEKVRRRIADLEATDAEFL
MAGWEAAAMGADGPVAAEGLDLEASSYRSYESLEVSASKSDVRWWTFAPPGMFEASEEAT
LPLDFEAGPAPRGELPKIDAMMAQLLAHTTGGGRAAFIAPTQGAIKRMVDRFAEKGIPTH
VATPGWEPTPGQVTLYHALSHAGLVFPKVRKHRDGAAMPLVVITETDLTGNRVGDIAGRN
VDLQNAATRWILWRWSQGIWWFMKPTALVVL

>RXN00833 TRANSLATE of: rxn00833.seq check: 7757 from: 1 to: 495
MAKTHFQGNETATSGELPQVGDNLAEFNLVNTELGEVSSKDFQGRKLVLNIFPSVDTGVC
ATSVRKFNEAAASLENTTVLCISKDLPFALGRFCSAEGIENVTPVSAFRSTFGEDNGIVL
EGSPLKGLLARSVIVVDENGKVAYTQLVDEIFTEPDYDAALAGLN

>RXN00937 TRANSLATE of: rxn00937.seq check: 2481 from: 1 to: 372
MATIDVTEETFESTVTGDGIVLVDAWASWCGPCRQFAPTYEKVSETHTDATFAKLDTEAN
QGLAAALQIQSIPTLMVFRDGIMVYREAGTMPAPALDDLVNQVKALDMDDVRRQVAEQQG
SAEA

>RXN00966 TRANSLATE of: rxn00966.seq check: 3319 from: 1 to: 540
MTNPSEGTTPLAFRYTPELANKIEGEWQNYWTDNGTFNAPNPVGDLAPADGKALPEDKLF
VQDMFPYPSGAGLHVGHPLGYIATDVFARYNRMLGKNVLHTLGYDAFGLPAEQYAIQTGT
HPRTTTMANIENMKRQLGALGLGHDSRRAVATTDPEFYKWTQWIFLQIFNSWFDAEQQKA

>RXN00975 TRANSLATE of: rxn00975.seq check: 760 from: 1 to: 1650
MTPADLATLIKETAVEVLTSRELDTSVLPEQVVVERPRNPEHGDYATNIALQVAKKVGQN
PRDLATWLAEALAADDAIDSAEIAGPGFLNIRLAAAAQGEIVAKILAQGETFGNSDHLSH
LDVNLEFVSANPTGPIHLGGTRWAAVGDSLGRVLEASSAKVTREYYFNDHGRQIDRFALS
LLAAAKGEPTPEDGYGGEYIKEIAEAIVEKHPEALALEPAATQELFRAEGVEMMFEHIKS
SLHEFGTDFDVYYHENSLFESGAVDKAVQVLKDNGNLYENEGAWWLRSTEFGDDKDRVVI
KSDGDAAYIAGDIAYVADKFSRGHNLNIYMLGADHHGYIARLKAAAAALGYKPEGVEVLI
GQMVNLLRDGKAVRMSKRAGTVVTLDDLVEAIGIDAARYSLIRSSVDSSLDIDLGLWESQ
SSDNPVYYVQYGHARLCSIARKAETLGVTEEGADLSLLTHDREGDLIRTLGEFPAVVKAA
ADLREPHRIARYAEELAGTFHRFYDSCHILPKVDEDTAPIHTARLALAAATRQTLANALH
LVGVSAPEKM

>RXN00985 TRANSLATE of: rxn00985.seq check: 4212 from: 1 to: 2709

MVCVTDQNNETTSQNRADKLPKSWDPKAVEADLYQGWVDAGYFTADPASDKPGFSIVLPP
PNVTGQLHMGHALDHTLMDALARRKRMQGFEVLWLPGMDHAGIATQTKVEEMLKETEGKT
RYDYDREEFIAKVWEWKQEYGGKIGEQMRAIGDSVDWSRERFTLDDGLSRAVQTIFKKLF
DAGLIYQANRLVNWSPVLETAVSDIEVIYKDVEGELVSIRYGSLNDDEPHVIVATTRVET
MLGDVAVAVHPDDERYKDLVGQTLPHPFRDDLSLKVVADDYVDPEFGSGAVKITPAHDPN
DYALGLRHNLDMPTIMDKTGRIADTGTQFDGLTREEARIKVREELAAQGRIVKEIRPYVH
SVGHSERSGEAIEPRLSLQWFVKVEELAKMSGDAVREGDTTIHPKSLEPRYFDWVDNMHD
WTISRQLWWGHRIPIWYGPNDEIICVGPDEQAPEGYVQDPDVLDTWFSSALWPFSTMGWP
EKTPELEKFYPTSVLVTAYDILFFWVARMMMFGTFAAKETPELLGEGKDGRPQVPFTDLF
LHGLVRDEHGRKMSKSLGNGIDPMDWVENYGADALRFTLARGANPGVDLPVGEDSAQSSR
NFATKLFNATKFALMNGAVSEGLPAREELTDADRWIVDLLEQVRLDVDAYLDNYQFAKAN
EELYHFAWNEFCDWYLEIAKVQIPREGTSAQGENTQKVLGHVLDALLRLLHPAMPFVTEV
LWQALTDRTSIVVASWPTAADTNGGVAVDADAARRIGDVEKLVTEVRRFRADQGVKPSQK
VPARLDFVACDLQDLEDSVRSLVRIEQPEDDFAASASLEIRLSQATITVELDTSGTVDVA
AERKRLEKDLANAQKELETTAKKLGNEAFLSKAPDAVVDKIRGRAQIAQEEVERINKRLE
ELA

>RXN01061 TRANSLATE of: rxn01061.seq check: 5052 from: 1 to: 1038
ISRYREQFCNIENERYWTGPRPETHGPNDPGGVDLYVGGVEHAVLHLLYARFWHKVLFDL
GHVSSKEPYRRLYNQGYIQAFAYTDSRGVYVPADDVEEKDGKFFYQGEEVNQEYGKMGKS
LKNAVAPDDICNNFGADTLRVYEMAMGPLDTSRPWATKDVVGAQRFLQRLWRLVVDENTG
EVLTRDEVLTDDDNKQLHRTIAGVRDDYTNLRVNTVVAKLIEYVNYLTKTYPDTIPAGAV
LPLIVMVSPIAPHIAEELWKKLGHDDTVTYEPFPTFEEKWLTDDEIELPVQVNGKVRGRI
TVAADASQEQVIEAALADEKVQEQISGKNLIKQIVVPGRMVNLVVK

>RXN01284 TRANSLATE of: rxn01284.seq check: 2030 from: 1 to: 567
VAKAKFERTKPHVNIGTIGHVDHGKTTTTAAITKVLADTYPELNEAFAFDSIDKAPEEKE
RGITINISHVEYQTEKRHYAHVDAPGHADYIKNMITGAAQMDGAILVVAATDGPMPQTRE
HVLLARQVGVPYILVALNKCDMVEDEEIIELVEMEVRELLAEQDYDEEAPIVHISALKAL
EGDEKWGKQ

>RXN01345 TRANSLATE of: rxn01345.seq check: 9398 from: 1 to: 1452
MRFGLDLGTTRTIAAAVDRGNYPIVTVEDSLGDTHDFIPSVVALKADRIVAGWDAIEVGQ
DHPSFVRSFKRLLSEPNVTEATPVYLGDHVHPLGAVLEAFAENVVTALRAFQTQLGDTSP
IEVVIGVPANSHSAQRLLTMSAFSATGITVVGLVNEPSAAAFEYTHRHARTLNSKRQAIV
VYDLGGGTFDSSLIRIDGTHHEVVSSIGISRLGGDDFDEILLQCALKAAGRQHDAFGKRA
KNTLLDESRNAKEALVPQSRRLVLEIGDDDITVPVNKFYEAATPLVEKSLSIMEPLIGVD
DLKDSDIAGIYLVGGGSSLPLVSRLLRERFGRRVHRSPFPSGSTAVGLAIAADPSSGFHL
RDRVARGIGVFREHDSGRAVSFDPLIAPDTDSATVAKRCYKAVHNIGWFRFVEYSTVSED
GSPGDISLLSEIKIPFDSSITDVDATEISRFDGPEVEETITVNDNGVASISIKILGGVTV
EHTI

>RXN01404 TRANSLATE of: rxn01404.seq check: 9645 from: 1 to: 999
QKMSTSRPTIYDVAKAAGVSKSLVSLVLRGSPNVSKESEAAVKTAIKKLNYQPNRAASDL
AAKRTQLIAVLIDDYSNPWFIDLIQSLSDVLTPKGYRLSVIDSLTSQAGTDPITSALSMR
PDGIIIAQDIPDFTVPDSLPPFVIAGTRITQASTHDSVANDDFRGAEIATKHLIDLGHTH
IAHLRVGSGAGLRRFESFEATMRAHGLEPLSNDYLGPAVEHAGYTETLALLKEHPEVTAI
FSSNDITAIGALGAARELGLRVPEDLSIIGYDNTPLAQTRLINLTTIDDNSIGVGYNAAL
LLLSMLDPEAPHPEIMHTLQPSLIERGTCAPRG

>RXN01490 TRANSLATE of: rxn01490.seq check: 1933 from: 1 to: 891
MNAPAPKPGLVIVDKPAGMTSHDVVSKLRRAFSTRKVGHAGTLDPMATGVLVVGIERGTR
FLAHMVASTKAYDATIRLGAATSTDDAEGEVISTTDASGLDHSTILAEIVNLTGDIMQKP
TKVSAIKIDGKRAHERVRDGEEVDIPARPVTVSVFDVLDYHVDGEFYDLDVRVHCSSGTY
IRALARDLGNALQVGGHLTALRRTEVGPFTLNDATPLSKLQENPELSLNLDQALTRSYPV
LDITEDEGVDLSMGKWLEPRGLKGVHAAVTPSGKAVALIEEKGKRLATVFVAHPNTL

>RXN01496 TRANSLATE of: rxn01496.seq check: 8990 from: 1 to: 3012
VPGKLRVHELAKQLGITSKELLATLKDKGEFVKTASSTIEPPVVKRMQEHYGSSGSDKSD
TAAKPAAAKPAAPKPAASAAPKPGAPAKPAAPAAKPAPAAPSAASAAKPGAAPKPGVQAK
PAAAAKPGAPAKPAAPAAPSAAKSGSASKPAAAAKPAFSGPTPGDASKKAEPAAKPGAEA

PRPGGMPRPMGKPAPKPGARAPRVANNPFSTGGGERPAPRPGGGPRPGGGPRPGGGPRPQ
GQGRPGGQRDGQRDGQRDGQGNRGGQRQGAGAGGPRPQGGPRPQGGSRPQGGSAQGAQGA
PSQERQGGGRRPSPAMMPPTPGQMPAKAPGKGGRGGQAGGGAGGGFNRGGGTGGGAGRGG
RRGGTAGAFGRPGGAPRRGRKSKRQKRNEYESMQAPNVIGGVRLPDGKGATIRLARGASL
ADFADKIGADAAALVQALFNLGEMVTATASVSDETLQLLGEEMNYKVQVVSPEDEDRELL
ESFDLQFGEDEGGEADLAKRPPVVTVMGHVDHGKTRLLDTIRKANVGSDEAGGITQGIGA
YQVKVNVEDTERTITFLDTPGHEAFTAMRARGAKSTDIAVLVVAADDGVMPQTVEAINHA
KAADVPIVVAVNKIDKPEASPEKIRGQLTEYGLIPEEYGGDTIFVDISAKQGLNIDELLA
SVCLTADAELDLVANPEMDAQGVAIEAHLDRGRGPVATVIVQRGTLRVGDSIVAGDTYGR
VRRMVDEYGRDVEEAGPSRPVQVQGLNGVPGAGDNLLVVEDDRIARQIANQRNARKRNAL
AARSRKRVSLEDLDSVLKEHSTLNLILKGDNAGSVEALEEALLKIEMDDEVQLNIIDRGV
GAVTQTNVTLAAASDAVIIAFNVRAEGKATEEANAEGVDVRYYTIIYRAIEEVEAALKGM
LKPIYEERVIGHAEIRAIFKASSVGLIAGCMVEDGKVRRNATVRIIRDGNVIAENAKIVS
LRREKDDATEVSAGYECGMVLSYPDISVDDKIEVYEMVEVPREA

>RXN01541 TRANSLATE of: rxn01541.seq check: 7782 from: 1 to: 777
MTTPHSHRAPRLASTVIIARESADSGTLEFFIQQRQSTMAYAANAVVFPGGGVEDSDYPF
MLPHRDQHMSPEHIKHHASRLHMDSETMAAHISAARREVWEETGVDLGNYNHELIPIDRW
ITPDIPAFRRRYDTATFVLILSKDSTNAALQHQHQTTEATHSYWATAEEELLTQWSTGHLN
LLLPTWWHINQLNHLHTLNQLYSFAQRTHNPQHTPPTVFANWTAPADEAAMQHYGFPDPD
AYFDHATIAGKHHTLITRK

>RXN01559 TRANSLATE of: rxn01559.seq check: 3150 from: 1 to: 1842
VLIVVGVYALVLLTGDRSATPKLGIDLQGGTRVTLVPQGQDPTQDQLNQARTILENRVNG
MGVSGASVVADGNTLVITVPGENTAQAQSLGQTSQLLFRPVGQAGMPDMTTLMPELEEMA
NRWVEYGVITEEQANASLEEMNTAVASTTAVEGEEATEPEPVTVSATPMDEPANSIEATQ
RRQEITDMLRTDRQSTDPTVQIAASSLMQCTTDEMDPLAGTDDPRLPLVACDPAVGGVYV
LDPAPLLNGETDEENGARLTGNEIDTNRPITGGFNAQSGQMEISFAFKSGDGEEGSATWS
SLTSQYLQQQIAITLDSQVISAPVIQSATPVGSATSITGDFTQTEAQDLANNLRYGALPL
SFAGENGERGGTTTTVPPSLGAASLKAGLIAGIVGIALVAIFVFAYYRVFGFVSLFTLFA
AGVLVYGLLVLLGRWIGYSLDLAGIAGLIIGIGTTADSFVVFYERIKDEIREGRSFRSAV
PRAWESAKRTIVTGNMVTLLGAIVIYLLAVGEVKGFAFTLGLTTVFDLVVTFLITAPLVI
LASRNPFFAKSSVNGMGRVMKLVEERRANGELDEPEYLKKIHAKNAAADKASTDNSSTDN
SEAPGTDTNQEEEK

>RXN01583 TRANSLATE of: rxn01583.seq check: 2692 from: 1 to: 2343
VETIEELTEFKKPIRHCVNVGDANGTGELQSIVCGARNFKEGDTVVVSLPGAVLPGDFA
ISARETYGRMSAGMICSASELGLADKQNSGIITLDPSYGEPGEDARQALGLEDTVFDVNV
TPDRGYALSARGLTRELASAFSLTFTDPAIEPAVAGIEVKVPAVEGSLINVELREETKAI
RFGLRKVSGIDPAAESPFWMQRELMLSGQRPVNAATDVTNYVMLLLGQPMHAFDAAKVTG
DLVVRNATAGEKFETLDHVKRTLNEEDVVITDDNGIQSLAGVMGGLTSEISDTTTDVYFE
AATWDTITVARTSRRHKLSSEASRRFERGVDPAIVEIALDIAATLLVEIAGGTVDAGRTL
VGDVPAMQPITMKVTRPSELAGVDYSAETVIARLEEVGCTVAVSGDTLEVTPPTWRGDLT
MSADLVEEVLRLEGLEAIPTIIPTAPAGRGLTDAQKRRRAVGHALAYAGYAEIIPSPFMD
PEVFDVWGLAADDERRKTVSVLNPLEAERNVLSTSLLPSMLDAVKRNVARGHNDFSLFGL
QQVAFEHGSGVSPMPSVASRPEESVVAELVDSLPNQPLHVATVGTGNIEFEGPWGKGRAY
TFADAIESARAVARAAGVTLELANADALPWHPGRCAALLIDGTPVGYAGELHPQILEKAG
LPARTCAMELDLSALPLVENLPAPVLSSFPALHQDIALVVDETIPAEDVRAVVEAGAGEL
IETVELFHVFRSEQRGENKKSLAFSLRFRAAGRTLTDEEANEARLQAAELAKEKFNAEMR
G

>RXN01670 TRANSLATE of: rxn01670.seq check: 7045 from: 1 to: 807
MPEGHVIHRLAGELTKNFGDTILDATSPQGRFTSEAAIINGHRIAVAEAYGKHLFVEFDA
DHPEHILYIHLGLIGTLQFEPAEETRGQIRLHLSDGEIAANLRGPQWCRLITDAERTQAI
GKLGADPIRDDADPEPIRIKVQRSGRSIGSLLMDQKLFAGVGNIYRAETLFRLGISPFTI
GKDITTAQFRSIWADLVGLMKDGVVTGRIDTVRPEHTPEAMGRPPRKDDHGGEVYTYRRT
GQECFLCATPIKEQVMEGRNLFWCPGCQR

>RXN01671 TRANSLATE of: rxn01671.seq check: 7692 from: 1 to: 1149
MNHVVNFASHLEDAALKQAEATATMPFIYPHVALMPDAHFGLGSSVGTVFGTKGAIIPAA
VGVDIGCGMIGVCTNYTASDLEGRDLVTLRDYIERVIPLSPGNYNSTTLKETAKVKVAEL

EELAERDGVDLSHSPTWKRQLGSLGGGNHFIELCLDELDRVWMFLHSGSRGVGNKIAQKH
IKIAQAECKNEELPDKDLAYLTEGTEEFESYIKELNWAQRFAFLNREEMMDRFARELGFF
VDKQLEEVERINCHHNYTVQEEHYGETIWLTRKGAVLADEGTPALIPGSMGTASYVGSGK
GNAEALRSAPHGAGRRMSRNQAKKRFSTADLDSRMAGIVYRPGKEWIDEIPDAYKDIDQV
MADAADLVTIRHKLRQIVNVKGT

>RXN01676 TRANSLATE of: rxn01676.seq check: 7951 from: 1 to: 756
MILHGVVFYAGLLVLLVPLGLGAGILGELFITQRQTIIVVSSIVLIILGFVQIFGGGFDF
GKALPGLDRLQSKATVTSGLGKSFLLGMTSSIAGFCSGPILGAVLTLAATSGNSITSALI
LSAYGAGMVLPLMAIAALWAKLGQRGQQMLRGREFTFLGRQWHIVSVISGALIIAVGILF
WSTNGLVSMPELVPMDTQIWLQEATFSLGSPLFDIALIIVAAGLFLYFWNKRQKRKEEAQ
RPKESGWVINPR

>RXN01680 TRANSLATE of: rxn01680.seq check: 4368 from: 1 to: 411
MAGHTHKTHRTAYKQLEALARNGHLFTYIDPPAEVDGVVKSTTNCLEGGINAQIKALARN
HRGMFDEHQRIAVDWWLLMHTQLPGDPVEIARQQNWGQDGLANVPDLIQQEQPHDHYGRP
VTYDTGIDATTTRRKSK

>RXN01704 TRANSLATE of: rxn01704.seq check: 8117 from: 1 to: 1077
RGIGNAGKGVKVTTASADRVDSRCPAAAAGAGCCDYAELNPTVELEIKSRVLRDQLERIG
GIDELPEFELQDLEPTAGWRTRVRLGVDASGRAGFRKLKSNELVTEVACSQVVPELLEGL
VGEGARRFTPGVEIIAAIDDAGQRHVVESRKAPRGRRTETVLKVLEGTGEVEQKVGDYTW
KFPVSSFWQAHTKAPAAYSEFIAEALTGLELVDVDKRGPVAWDLYGGVGLFAPIITSKLQ
AAVHSVELSPGSAEAGEEALAGLPVTFHTGRVEGMASQLPSPNVVVLDPPRTGAGSDVLK
SIAEAKPQLVIHIGCDPATFARDVADWKLNGYEMDQLAVFNAFPGTHHFETIGVFVRVS

>RXN01724 TRANSLATE of: rxn01724.seq check: 2602 from: 1 to: 1320
RATQPSAPVEQAQEAPAQTSTAPASAPSEETPAAPARRGRRRVTTTATTPEPAAPAQSQP
AEAQPAQTQAAQQEELPVAAKESAPATENTQGQAQGQAQGQAQGDEHDDRFESRSAARRA
RRNRQRQIHRDGDDNANANTESEQNTPAQNATAQAESEQTAAPAQAEAAEQNQNDNSESS
ENRSDNYRNNNRRSRNNRNNRNYRDNNESSDNAGQSSNDDADNNQARSEDNNDDRRSRNN
RNNDRNDRNDRNDRDNDDNDDRRNRRGRRNRRGRNDRNDRDNRDNRDNRDNSNDGDNNQQ
DELQQVAGILDIVDHNVAFVRTTGYHAAPSDVFVSNQLIRRMGLRSGDAIEGQVRMNQGG
GNHNNHGRNRQKYNNLVRVEMVNGLPAEETRNRPEFGKLTPLYPNQRLRLETEQKILTTR
VIDLIMPIGKGQLCFDCVAT

>RXN01725 TRANSLATE of: rxn01725.seq check: 6605 from: 1 to: 207
LIVSPPKAGKTTILQNIANAISTNNPECYLMVVLVDERPKEVTDMQRSVNGEVISSTFDR
PPSEHTAVA

>RXN01730 TRANSLATE of: rxn01730.seq check: 9668 from: 1 to: 1704
VLRTHLSGELRKENAGQSVTLTGWVNRRRDHGGVIFIDLRDRTGIAQVVFRNEDVAERAH
ALRSEFVLRVTGVVEERPEGSQNPNLASGDIEVSVTEFEVLNESAPLPFQIEDSSSAGEV
GEETRLKYRYLDLRRPVQANALRLRSAANKAARTVLDSHDFTEIETPTLTRSTPEGARDF
LVPARLRPGTFYALPQSPQLFKQLLQVAGMERYYQIARCYRDEDFRADRQPEFTQLDVEM
SFVDQDDVIALGEEIISEVWKLIGYEIKTPIPRMTYADAMRRYGSDKPDLRFDIEITECT
EFFQDTTFRVFKNEYVGAVVMTGGASQPRRQLDAWQEWAKQRGAKGLAYILVGEDGELSG
PVAKNITDAERAGIAAHVGAQPGDCIFFAAGDTKSSLALLGAARGEIAKKLDLIKEGDWA
FTWIVDAPMFEPAADATASGDVALGNSKWTAVHHAFTSPKPEFLDNFDTNPGDALAYAYD
IVCNGNEIGGGSIRIHQRDVQERVFEVMGITGEEAREKFGFLLDAFAFGAPPHGGIAFGW
DRIVSLLGGFDSIRDVIAFPKSGGGIDP

>RXN01733 TRANSLATE of: rxn01733.seq check: 4482 from: 1 to: 1182
MHIRSLELRDYRSWPELKVDLEPGITVFIGRNGFGKTNIVEAIGYLAHLSSHRVSSDAPL
VRAHAENARVSAVAVNQGRELAAHLLIKPHAANQASLNRTKVRTPRELLGVVKTVLFAPE
DLALVKGEPAERRRYLDDIIATRQPRMAGVKADYDKVLKQRNALLKTATIALRRGYGTEE
GAAALSTLDTWDGQLARLGAEVMAARFALLNELGPKIYEAYTTIAPESRPAAVNYKTTID
QGLSQFSEFDAGIIEATLLTELAAKRQREIERGSSLVGPHRDDVDLMLGDQPAKGFASHG
ETWSFALSLRIAEFNLLKSDGTDPILILDDVFSELDAGRREKLVGIAQEVEQVLITAAVH
DDLPENLKKVLTAQHTVTVQDTGTGRISLLDVQP

>RXN01784 TRANSLATE of: rxn01784.seq check: 6464 from: 1 to: 582
MMTERGVPVDHTTIYRWVQKYALELDKQTRWYRQVPDWQASSWRVDETYIRVGGTWCYLY
RAITAGGQTLEFYLSPKRNVAAAKRFLAKTLRSNTTAGSPRVINTDKAPALAKAISELKA
EGICPQTVEHRQVKYLNNVIEGDHGRLKRILGPKGAFKNRISAYRTLKGMEAMHSLRKGQ
GTMFDLTGTRTQTR

>RXN01795 TRANSLATE of: rxn01795.seq check: 439 from: 1 to: 597
VLIVGIRRDTGFDFKHPAPTHGPRGDMPYKTAGEALKGVKDVPTNNNHMKIMPRTVEVLK
RIPEGENFTAIPKDDPYYVKGMISHVYRRLHRDEPSKTLIAGGGGGTWGYHYEKNRALTN
RERARIQSFPDDFEFLGSNTEVRRQIGNAVPPVGMHAVGERLMNLYTGNYTPVDLEEQHA
YLQTLSIKERLALADQEAD

>RXN01837 TRANSLATE of: rxn01837.seq check: 8888 from: 1 to: 777
VSTNKERRQQALSQLEKEIKSRDRKEKTKPLTVVFASLAVILVVVGGIWYAATRSTEDEV
ITADETSTTAETPDYQPLALTRTTALGDSVTCEYPDAGEASKDVSKPATENVPATGTVTV
NLTTAQGNIGMELDRSVSPCTVNAVEHMASEGYYNDTVCHRITTSGIYVLQCGDPSSTGA
GGPGFSFANEYPTDEATDLTTPVIYERGTIAMANAGADTNGLPVLPQLRGFPTGTELHLL
RPDHRRRPCNPRRHRRSWH

>RXN01863 TRANSLATE of: rxn01863.seq check: 1675 from: 1 to: 1149
MNSVKLKQPVSIYNDPWESYNDVKEHGQLTLSNIEFTTTNLCNMRCSHCAVGYTLQTVDP
EPLDMDLIYRRLDEIPNLRTMSITGGEPMFSKKSIRNVVKPLLKYAHHRGIYTQMNSNLT
LPQDRYLDIAEYIDVMHISHNWGTTDEFANVGFGAMKKQPPLKAKLKLYEQMISNARTLS
EQGMFVSAETMLNQSTLPHLRKIHQEVVHDMKCSRHEIHPMYPADFASQLNVLTLAEMKK
TIHDILDFRDEDIWMLFGTLPVFPCLKDDEDQKLLSRLRNANNVTTRNDPDGRSRLNVNV
FTGNVIVTDFGDETGTISNIQKDKLTDVFDKWLSSDLAKSLNCHCSEFSCLGPNVLVKNM
YYPNMDFKDNERHMHKQPQIIQF

>RXN01872 TRANSLATE of: rxn01872.seq check: 8549 from: 1 to: 828
MGNDGGDLRIDDLRSFISVAQSGHLTETAQRLGIPQPTLSRRISRVEKHAGTPLFDRAGR
KLVLNQRGHAFLNHASAIVAEFNSAATEIKRLMDPEKGTIRLDFMHSLGTWMVPELIRTF
RAEHPNVEFQLHQAAAMLLVDRVLADETDLALVGPKPAEVGTSLGWAPLLRQRLALAVPA
DHRLASFSGQGELPLITAAEEPFVAMRAGFGTRLLMDALAEEAGFVPNVVFESMELTTVA
GLVSAGLGVGVVPMDDPYLSTVGIVQRPLSPPAYRE

>RXN01926 TRANSLATE of: rxn01926.seq check: 2379 from: 1 to: 741
LRSFYTPEQAIEREGDVWKAATEEAELLAADGAVHDQELFLNCTTSPLIFASAMLNFGVH
QILDTLCQLAPSPAGRDADPKALEAATSAMDDHRDTTDDFSGVVFKVQAGMDKNHRDTLA
FMRVVSGEFDRGMQVTHSQSGRSFSTKYALTVFGRTRSTVETAFPGDIVGLVNAGALAPG
DTIFEGRKIQYPPMPKFAPEHFRILRAKSLGKYKQFRKALEQLDSEGVVQILKNDLRGDA
NPGHGRC

>RXN01938 TRANSLATE of: rxn01938.seq check: 4407 from: 1 to: 1428
MITRLSTLFLRTLREDPADAEVPSHKLLVRAGYIRRVAPGIYSWLPLGLRAVRNIEAVVR
EEMDAIGGQELLFPTLLPREPYETTQRWTEYGDSLFRLKDRKGADYLLGPTHEEMFAATV
KDLYNSYKDFPVTLYQIQTKYRDEERPRAGVLRGREFVMKDSYSFDISDAGLDESYAKHR
AAYQRIFDRLGLEYAICQATSGAMGGSASEEFLAVSENGEDTFVRSTSGNYAANVEAVVT
QPGVERDIEGLPEPVTYETPVSETIDALVDWANSIDVQIEGREVTADDTLKCIVVKVREP
GAEEAELTGILLPGDREVDMKRLEASLEPAEVELAVESDFADNPFLVKGYVGPVGLAKNG
VKVLADPRVVTGTSWITGADEKERHVVGLVAGRDFTPDGFIEAAEIKEGDPAPAGEGTLT
LARGIEIGISSSSAASTPKPSTSKSWTKTASAPSQPWALRARCHPPARRPGRTAPR

>RXN01969 TRANSLATE of: rxn01969.seq check: 287 from: 1 to: 366
LWAYDKAYGALKLAWLAYQAIIDCYQMGNKREAKKKMRTIIDQLRVLKGPNKELAQLGRS
LFKRLGDVLAYFDVGVSNGPVEAINGRLEHLRGIALGFRNLNHYILRCLIHSGQLVHKIN
AL

>RXN02002 TRANSLATE of: rxn02002.seq check: 9539 from: 1 to: 378
MSNANSDTTAAEAHRRRTFAVIAHPDAGKSTLTEALALHAHIISEAGATHGKAGRKATVS
DWMEMEKDRGISIASSALQFEYAPEGHAGEPFMINLVDTPGHADFSEDTYRVLMAVDAAV

MLMHSV

>RXN02004 TRANSLATE of: rxn02004.seq check: 647 from: 1 to: 207
RVGRLMRQNGILIIRSRKFKRTTGSDHTFNIAPNFLQQDFMASRPNQKWAGDITYVWTRE
GLGLSGRHS

>RXN02267 TRANSLATE of: rxn02267.seq check: 5927 from: 1 to: 873
VQKWGLSFVERIVIVNNVQQFHRFFDDSAVYYPCFVPLDRAIGEHFDRQNKPMSRFIGTL
ILPLAKLEEAAQYTGDEVLRVSAVISTDGLADLRRDFYELPNIDIASVEIKLVGAALTNT
AWLGDVEKLIQQHRNTFVWVEIPTALVTADIVRKLRHMGAGLKYRTGGDREELFPSPQDL
VTVLRTAIDAALPFKLTAGLHRALRYRDEKTGRLHFGFLNIAAAVATLRAGKGEAEALKI
LEGDDAAPLIHALQSGENWRDSFRSFSTCNVVEPLNTLIDLDVLAEGDVHP

>RXN02280 TRANSLATE of: rxn02280.seq check: 171 from: 1 to: 1824
MQESSRDNFQVDLGGVVDLLSRHIYSGPRVYVRELLQNAVDACTARSEQGEEGYEPSIRI
RPVTKDRATFSLVDNGTGLTAQEARELLATVGRTSKRDEFGLQREGRLGQFGIGLLSCFM
VADEITMVSHAEGASAIRWTGHADGTFNLEILGDDATDVIPVGTTVHLTPRPDERTLLTE
NSVVTIASNYGRYLPIPIVVQGEKNTTITTSPVFAKDTDQQHRLYAGRERLGKTPFDVID
LTGPGIEGVAYVLPEAQAPHMSRRHSIYVNRMLVSDGPSTVLPNWAFFVECEINSTDLEP
TASREALMDDTAFAATREHIGECIKSWLINLAMTKPHRVREFTAIHDLALRELCQSDADL
AETMLGLLTLETSRGRISIGEITTLSITEDVSLQLATTLDDFRQLNTIARPDTLIINGGY
IHDSDLARLIPVHYPPLTVSTADLRESMDLMELPPLQDIEKAKALDAQVTESLKDFQIKG
ATRVFEPADVPAVVIIDSKAQASRDRNETQSATTDRWADILATVDNTLSRQTANIPQDQG
LSALCLNWNNSLVRKLASTDDTAVVSRTVRLLYVQALLSSKRPLRVKERALLNDSLADLV
SLSLSSDI

>RXN02287 TRANSLATE of: rxn02287.seq check: 4446 from: 1 to: 552
VYSISETIARTLMPRTDHVFDLMGNGNAWFVDALERLGRGIITVRPTVETVAAADTYHRV
TRRPAVATTTYGAGFTNTMTTLADVALSRIPLLLVVGTAPSAGPRCFDIDRQGLARAVGV
ETFTVHADDVAAVTLQAWNNTPENTHVILEIPYDLAAATATDPTVTTYLLRPGFQKLPMS
PTLS

>RXN02291 TRANSLATE of: rxn02291.seq check: 8232 from: 1 to: 654
VVHLPNFLGLAEQKALVAQARDLAREVVGTPLAMVRPKLKSGQMSVHMLHLGKYWASNPY
RYVDVVDGFPVPPLPDSFVDLAHRALLSAGSLSNSLQSWSEAYRAEAALVNYYSPDASMG
MHQDANEESEAPVISLSIGDTGIFRLGGTLNRNKPWTDIPLMSGDLIVFGGANRQAFHGI
PSIEANTAPAGCGLKEGESTSRSANLHYKTPGRGMSRG

>RXN02325 TRANSLATE of: rxn02325.seq check: 7224 from: 1 to: 867
MDHAHDSCSPTLRRDLEVTGQLQPEKAVDLAAPHEGKVANITKVTSSNMEHTITQASKAK
EVVVLIGHSLLPTFQDLEKDILHFQAGNKGRFSVAIVDPDRSADVVARFRPKQIPVAYVV
KDGASIAEFNSLNKEPVAQWLDHFVSRETIPNEKEGDVDKQIDPRLWRAAELVNAGDFRA
ALALYEQLPQDATVKRAHAAVSVLARMSVADRGEDPIEKSRRDPDDVNKALAAADMYVLM
NQPDTALAHLAALLPKPEAARRIVELLNLFDPLDLVALEIRAQVGNAMS

>RXN02386 TRANSLATE of: rxn02386.seq check: 6167 from: 1 to: 459
MAALAENYQTPAPSSQVVVSVVGHVAKPGLVTLAEGSRVADALAIAGALPDADLTALNLA
QLLVDGTQIHVLAIGEVQPISVDAAATSASGLISLNTATVADLVTLPGVGEKTAQAIIDF
RESNGGFSTVEDLLQVKGIGPSKFEQISGLVSP

>RXN02388 TRANSLATE of: rxn02388.seq check: 380 from: 1 to: 1662
MIEVRLVPVAAVMWMAVAALIINGSWVLSVGIVGIAIIAACVFKHWGQAVVIAALGVGAV
VMAALRISSAKAFEAPQTWVGTAETIKFLDSGDQLIGLRVEGYPAPIPVFYSGSDTIEKA
SLIAVSGRIKPDSFPGVGDLTISTEDIDQLEPTTGYSAWVNQVRDGFSQAVEETVGESSR
GLIPGMVLGDTRLQGSIEAQTYIDTGLSHLSAVSGSNVAIVVSSVVVLSYFLTAGPRIRV
VASLLSLVIFVSLVGFEPSVLRASVTGIVGLLAIINSSRMEPMHGLSLSVICLLFYDSNL
AVHYGFLLSCAATAGIVMLQPLLYRAIGPPLAVWKVPDIVVRAFAVSIAADLVTIPIIAL
MARQISLVAVLANVLVELAVPPITLLGLIAVLASLLPWPVEYPLLKIIEPFTWWIHHVAK
WCQQLPNSTLEISAGWAGIAWACMAAVWVVVIIYKGYVRTLAVCCVCFFLFGAWNNRLPA
QIDPTELRFVIIADDSELTDVPEHAELIIVEDPHGSMSDRPIVTREGIPVLYPYRDGEVS
LHIDGTQHAADGRF

>RXN02416 TRANSLATE of: rxn02416.seq check: 4089 from: 1 to: 2829
VRGAREHNLKGVDIDLPRDSMVVFTGLSGSGKSSLAFDTIFAEGQRRYVESLSSYARMFL
GQMDKPDVDLIDGLSPAVSIDQKSTNRNPRSTVGTITEVYDYLRLLYARAGTAHCPVCDA
RVERQTPQQMVDQILGMEEGLKFQILAPVVRTRKGEFVDLFADLASQGYSRVRVDGEVHQ
LSDPPKLEKQIKHDIDVVVDRLQVKASQKQRLTDSMETALRLADGVAVLEFVGLEEDDPN
RLRRFSEKMSCPNGHALTVDELEPRAFSFNSPYGACPACDGLGVRTEVDIDLIIPDPDAP
ATKAVQPWNSSPNHSYFEKLIEGLAKALGFDPETPYSELTAAQKKALVYGSKEEVSVRYK
NRYGRVRSWTAPFEGVMGYFDRKLEQTDSETQKDRLLGYTREVPCPTCKGARLKPEILAV
RLDSGSHGALSIAGLTALSVHEAFEFLDNLTLGKREEMIAGAVLKEIHARLKFLLDVGLS
YLTLDRAAGTLSGGEAQRIRLATQIGSGLAGVLYVLDEPSIGLHQRDNQRLITTLEHLRD
IGNTLIVVEHDEDTIRRADWLVDIGPRAGEFGGEVVYQGEPKGILDCEESLTGAYLSGRR
TLGVPDTRREIDKERQLKVVGARENNLQGIDVKIPLGVLCCITGVSGSGKSTLVNQILAK
VLANKLNRARQVPGRAKRVEGLEHLDKLVQVDQSPIGRTPRSNPATYTGVFDKVRNLFAE
TTEAKVRGYKPGRFSFNIKGGRCEACQGDGTLKIEMNFLPDVYVPCEVCDGQRYNRETLE
VKYKGKNIAEVLGMPISEAADFFEPITSIHRYLATLVDVGLGYVRLGQAATTLSGGEAQR
VKLAAELQKRSNGRTVYILDEPTTGLHFEDIRKLMMVIEGLVDKGNSVIIEHNLDVIKA
ADWIVDMGPEGGSGGGTVVAEGTPEQVAEVAGSYTGQFLKELL

>RXN02431 TRANSLATE of: rxn02431.seq check: 2412 from: 1 to: 876
DPLPVGALWGVGPVTGSKLASMGVETIGDLAALTQKEVEISLGATIGISLWNLARGIDDR
PVEPRAEAKQISQEHTYEKDLLTRQQVDAAIIRSAEGAHRRLLKDGRGARTVSVKLRMAD
FRIESRSYTLSYATDDYATLEATAFRLARYPGEVGPIRLVGVSFSGLEESRQDILFPELD
QQIIVPPAPDTDYEVGVQSSSSSESTQVEAPQDVALSMWCATQDVYHPEYGHGWVQGAGH
GVVSVRFETRSTTKGRTKSFSMDDPDLTPADPLDSLDWADWFAENGETGDDE

>RXN02462 TRANSLATE of: rxn02462.seq check: 3189 from: 1 to: 1818
MTKDVHYEVDERKKTVGVKEEGVEYVEDQLGIDNLYAPEHSQLVSYLNNAIKAQELFTRD
KDYIVRNGEVMIVDGFTGRVLAGRRYNEGMHQAIEAKERVEIKNENQTLATVTLQNYFRL
YTKLAGMTGTAETEAAELNQIYKLDVIAIPTNRPNQREDLTDLVYKTQEAKFAAVVDDIA
ERTEKGQPVLVGTVSVERSEYLSQLLTKRGIKHNVLNAKHHEQEAQIVAQAGLPGAVTVA
TNMAGRGTDIVLGGNPEILLDIKLRERGLDPFEDEESYQEAWDAELPAMKQRCEERGDKV
REAGGLYVLGTERHESRRIDNQLRGRSARQGDPGSTRFYLSMRDDLMVRFVGPTMENMMN
RLNVPDDVPIESKTVTNSIKGAQAQVENQNFEMRKNVLKYDEVMNEQRKVIYSERREILE
SADISRYIQNMIEETVSAYVDGATANGYVEDWDLDKLWNALEALYDPSINWTDLVEGSEY
GKPGELSAEDLRTALVNDAHAEYAKLEEAVSAIGGEAQIRNIERMVLMPVIDTKWREHLY
EMDYLKEGIGLRAMAQRDPLVEYQKEGGDMFNGMKDGIKEETVRQLFLSASSSSSKTRKS
LTNSEP

>RXN02543 TRANSLATE of: rxn02543.seq check: 6877 from: 1 to: 1854
MGRAVGIDLGTTNSVVSVLEGGEPVVIANAEGSRTTPSVVAFAKNGEVLVGQSAKNQAVT
NVDRTIRSVKRHIGTDWSVAIDDKNYTSQEISARTLMKLKRDAEAYLGEDVTDAVITVPA
YFEDSQRQATKEAGQIAGLNVLRIVNEPTAAALAYGLEKGEQEQTILVFDLGGGTFDVSL
LEIGDGVVEVRATSGDNELGGDDWDQRIVDWLVEKFQSSNGIDLTKDKMALQRLREAAEK
AKIELSSSQSANINLPYITVDADKNPLFLDETLSRAEFQRITQDLLARTKTPFNQVVKDA
GVSVSEIDHVVLVGGSTRMPAVTELVKELTGGREPNKGVNPDEVVAVGAALQAGVLRGEV
KDVLLLDVTPLSLGIETKGGVMTKLIERNTTIPTKRSETFTTAEDNQPSVQIQVFQGERE
IATANKLLGSFELGGIAPAPRGVPQIEVTFDIDANGIVHVTAKDKGTGKENTITIQDGSG
LSQDEIDRMIKDAEAHADEDKKRREEQEVRNNAESLVYQTRKFVEENSEKVSEDLKAKVE
EAAKGVEEALKGEDLEAIKAAVEKLNTESQEMGKAIYEADAAAGATQADAGAEGAADDNV
VDAEVVEDDAADNGEDKK

>RXN02651 TRANSLATE of: rxn02651.seq check: 4052 from: 1 to: 930
MNNRQSRTLPVPEGLAGMRVDAALSKLLGISRTVAAELATAGDVSVDGAVVGKSERLVAD
SMLDVLLPEPAAPLMPKEEIVPGLDILYSDDDVIAVNKPVGVAAHPTVGWEGPTVVGGLA
AAGFRISTSGPPERKGIVQRLDVGTSGVMVVAASERGYTVLKRAFRDRTVDKTYHALVQG
HPDPLTGTIEAPIGRHPSAGWRFAVTTEGKHAVTHYETLEAFQEATLLKIHLETGRTHQI
RVHFSALHHPCCGDPMYGSDPALSERLGLNRQWLHAVSLGFNHPADGRWMEIVSPYPTDL
QHALDVLREQ

>RXN02732 TRANSLATE of: rxn02732.seq check: 432 from: 1 to: 441

MSENYSKIVVGTDGSKSSLLAVERAARIAAAFDATLIIGCAYYESKEDASETLRQDSVTI
LGDDPARENLDKAADAARAVGATSIETEVRTGTPVEALMAIVNDHQADLLVVGNRGINYL
TGRLLGSVPADVARQSDCDVMIVHTVS

>RXN02736 TRANSLATE of: rxn02736.seq check: 2617 from: 1 to: 957
MIFELPDTTTQQISKTLTRLRESGTQVTTGRVLTLIVVTDSESDVAAVTESTNEASREHP
SRVIILVVGDKTAENKVDAEVRIGGDAGASEMIIMHLNGPVADKLQYVVTPLLLPDTPIV
AWWPGESPKNPSQDPIGRIAQRRITDALYDRDDALEDRVENYHPGDTDMTWARLTQWRGL
VASSLDHPPHSEITSVRLTGASGSTSVDLAAGWLARRLKVPVIREVTDAPTVPTDEFGTP
LLAIQRLEIVRTTGSIIITIYDAHTLQVEMPESGNAPSLVAIGRRSESDCLSEELRHMDP
DLGYQHALSGLSSVKLETV

>RXN02827 TRANSLATE of: rxn02827.seq check: 5045 from: 1 to: 423
MYEQQKILNEVSEKRLQAIKDFTELGSGFKIAMRDLSIRGAGNLLGAQQHGFIDAVGFDM
YSQMLSEAVXRKQGKNSQVEKXXVEIDXGVDAYLPETYVADXRQKIEIYKRIRELDSQEM
LDELEDDLLDRFGEXPEEVAH

>RXN02915 TRANSLATE of: rxn02915.seq check: 8269 from: 1 to: 378
MPKPLPPETRRKIIDFDPFAPNSPSIEEFCSRLKISRRSFYNIRNRYQQDANAALHSHSS
APITARRTYDESITSTLLSIRARLKAQGWEYGPISIRFEGIFTRELTAPIPSVSTIARLL
RAAGAV

>RXN02919 TRANSLATE of: rxn02919.seq check: 2536 from: 1 to: 534
VPVDHTTIYRWVQKYAPELDKQTRWYRQVPDWQASSWRVDETYIRVGGTWCYLYRAITAG
GQTLEFYLSPKRNVAAAKRFLAKTLRSNTTAGSPRVINTDKAPALAKAISELKAEGICPQ
TVEHRQVKYLNNVIEGDHGRLKRILGPKGAFKNRISAYRTLKGMEAMHSLRKGSGNDV

>RXN02938 TRANSLATE of: rxn02938.seq check: 1933 from: 1 to: 741
MRNYPDLPHDFPGQNTELTPAKAPVWMHRLLDRIHTGRMANPLDGAETLGDTDSEKRAAV
LMLFSGSETSFDLPNDASVLLTHRTPTMRSHAGQIAFPGGRIDPTDTNAVDCAFREAWEE
TGLDRRTATPLAQLNEVHIRATGYPVYPILGHWHTPSPVAVASPHETDEVLDAPLYDLID
PKNRLMVGWREWHGPAFRINDYIIWGFTGGLLSAILDTAGWATEWDTDRIFDLENTLSTS
RNNERMR

>RXN02949 TRANSLATE of: rxn02949.seq check: 1467 from: 1 to: 333
VSDEQNSGVGGTSRPTGKRQLSGASTTSTSSYEAKQVSTQKKSSGSDSKPGGGVISFLPE
VVGEVRKVIWPTARQMVTYTLVVLGFLIVLTALVSGVDFLAGLGVEKILTP

>RXN02963 TRANSLATE of: rxn02963.seq check: 2332 from: 1 to: 1308
MKSTGNIIADTICRTAELGLTITGASDAGDYTLIEADALDYTSTCPECSQPGVFRHHTHR
MLIDLPIVGFPTKLFIRLPRYRCTNPTCKQKYFQAELSCADHGKKVTHRVTRWILQRLAI
DRMSVHATAKALGLGWDLTCQLALDMCRELVYNDPHHLDGVYVIGVDEHKWSHNRAKHGD
GFVTVIVDMTGHRYDSRCPARLLDVVPGRSADALRSWLGSRGEQFRNQIRIVSMDGFQGY
ATASKELIPSARRVMDPFHVVRLAGDKLTACRQRLQREKYQRRGLSQDPLYKNRKTLLTT
HKWLSPRQQESLEQLWAYDKDYGALKLAWLAYQAIIDCYQMGNKREAKKKMRTIIDQLRV
LKGPNKELAQLGRSLFKRLGDVLAYFDVGVSNGPVEAINGRLEHLRGIALGFRNLNHYIL
RCLIHSGQLVHKINAL

>RXN02985 TRANSLATE of: rxn02985.seq check: 7956 from: 1 to: 333
MRLESYAMAKKVDTSNATPALALLTERQIPFELDVHDVDPKSSKGFALDASEVMGVEPEV
VFKTLMADIDGEHVVAIVPASRTLNLKQLAKAGKGKHANMMDRSRAQVVTG

>RXN02986 TRANSLATE of: rxn02986.seq check: 1309 from: 1 to: 138
VFLDESAILQERIYVSAGRRGWSLIIAPDDVLLATDGVYADIADHS

>RXN02988 TRANSLATE of: rxn02988.seq check: 6478 from: 1 to: 606
MSTKPTIVSTFSGCGGLDLGLQEVGFDPIWANDFSEEAVQTYKHNIGDHIVHGDITEIDP
FTDDTIPDGDLVTGGFPCQDFSMIWKRPGLDGKRGTLYQNFRDFVAAKKPKAFIAENVKG
LLTANQHKAIKTILKTSKLLSLATSSSLACTTSLNTVSHNSANVCSLLAFAVTPALISST

QLLPMALAVTCRIRLPAKRSKA

>RXN02989 TRANSLATE of: rxn02989.seq check: 5945 from: 1 to: 1140
MAPKKTATKATAAKGNDRQKALDAALALIEKDFGKGAVMRLGDENRPPIQTISSGNTAID
IALGIGGFPRGRIVEVYGPESSGKTTVALHAIAQAQKAGGIAAFIDAEHALDPDYARKLG
VDTDALLVSQPDTGEQALEIADMLVRSGAIDIIVIDSVAALTPKAEIEGEMGDSHVGLQA
RLMSQALRKMTGALYNSGTTAIFINQLREKIGVMFGSPETTTGGKALKFYASVRCDIRRI
QTLKDGQDAIGNRTRLKVVKNKVSPPFKIAEFDIMYGEGISRESSVIDLAVDNGIVKKSG
SWFTYEGEQLGQGKEKVRLSLKENPELTDELEDKIFKKLGVGKYAAASDELTDDPVELVP
NVDFDDEADTEADTEADAED

>RXN03033 TRANSLATE of: rxn03033.seq check: 9071 from: 1 to: 1158
VDEQRAFDQGLKEENTLITDLTTCARLSHNKALRLIKLSKSTAYYRNKPRPRPAPKPVLQ
AVPAPTAPGVEPTPEPWQGKEPAVSSVRQALAEHERQFIVDAITAYPQLSVSGVFNMLFN
KGIYRASLRTWWRVAKQHKLLHKDRVSALSPGKRSPTPRVKPRLEATQPGQVVCWDVTFL
PSLVRGKTYALHLAIDLFSRKIVGAKVAPTENTSTAVELLTQVLADNPGVVTVHSDNGSA
MTSTRVRRLLADHGVALSLIRPRVSDDNAFVESVFHTLKYRPFYPKVFASMDQARVWVEE
FVVYYNTVHPHSGVAGHTPQSVFDGSWRAAHRLRVQALDAHYRQFPQRYVGRPVVQEVAG
VVRLNGARDDGSVQERVGGVASLLSA

>RXN03035 TRANSLATE of: rxn03035.seq check: 9071 from: 1 to: 1158
VDEQRAFDQGLKEENTLITDLTTCARLSHNKALRLIKLSKSTAYYRNKPRPRPAPKPVLQ
AVPAPTAPGVEPTPEPWQGKEPAVSSVRQALAEHERQFIVDAITAYPQLSVSGVFNMLFN
KGIYRASLRTWWRVAKQHKLLHKDRVSALSPGKRSPTPRVKPRLEATQPGQVVCWDVTFL
PSLVRGKTYALHLAIDLFSRKIVGAKVAPTENTSTAVELLTQVLADNPGVVTVHSDNGSA
MTSTRVRRLLADHGVALSLIRPRVSDDNAFVESVFHTLKYRPFYPKVFASMDQARVWVEE
FVVYYNTVHPHSGVAGHTPQSVFDGSWRAAHRLRVQALDAHYRQFPQRYVGRPVVQEVAG
VVRLNGARDDGSVQERVGGVASLLSA

>RXN03038 TRANSLATE of: rxn03038.seq check: 812 from: 1 to: 726
MHSKEELTVRKGISRVLSVAVASSIGFGTVLTGTGIAAAQDSAFDYGMDPNMNYNPIDDI
KDRPEGLSNLPYFGSKLTSWGSSYATASSGVVTSALPQYTDPRYPLGKDDLPKATIDMEP
EVLARLERFVGVDGDRIRQINAYSPSMGRTIPLVWVVPEDNTVPGPTVYALGGGDGGQGG
QNWVTRTDLEELTSDNNINLIMPMLGSFSFYSDWARESQSMGCAQQWETLLMHELPEPLV
AA

>RXN03039 TRANSLATE of: rxn03039.seq check: 1469 from: 1 to: 630
ALPQYTDPRYPLGKDDLPKATIDMEPEALARLERFVGVDGDRIRQINAYSPSMGRTIPLV
WVVPEDNTVPGPTVYALGGGDGGQGGQNWVTRTDLDELTSENNINLIMPMLGSFSFYADW
AGESESMGGAQQWETFLMHELPEPLEAAIGADGQRSIVGMSMSGGSVLNFATHDPNFYSS
VGSFSGCAETNSWMGRRWHRSHCLQRQCRA

>RXN03040 TRANSLATE of: rxn03040.seq check: 6898 from: 1 to: 309
MSXGDNAPIDEDAFKNRVLVGFEIEAMSNTCTHNLKAATDQMGIDNINYDFRPTGTHAWD
YWNEALHRFFPLMMQGFGLDGGPIPIYNPNGVTSSESSXRTVF

>RXN03049 TRANSLATE of: rxn03049.seq check: 1664 from: 1 to: 942
MVHMVFGDMNTDRAAQAYIIVITTIVMVVLFWIVLRYWSLADRARAQRFTASITEIGRKI
FLNRLRPRMSRQNTYTDKDISQFHWTNGLPPTDDESPEWIAARDNEWEGYTITLGDDPNG
TEKTITLDDLRELPQTSYVAVHTCMQGWSATARWTGVRLRDVLCHDLVHTLDLHHRHSPR
LLTIEIIPKPLPPETRCKIIDFDLFAPNSPSIEEFCSRLKISRRSFYNIRNRYQQDASAA
LHPRSSAQITSRRTYDESITSILLAIRAPPESPRMGXRXDLYXIRRHXHRGTDCTDSIRL
NYRLLVTRCRSSRK

>RXN03051 TRANSLATE of: rxn03051.seq check: 1794 from: 1 to: 735
MRSDVIELPEGVSKEKADQLEVAEARLNEGARLMATTGCEVMWPTGFSVCGRILDTYRQV
GGQLSWLGPPKSNELTNPDGVGKRSEFFGGAIYWHPDTGAYAVTLDGLRQWGTLNWESGP
LGYPTSGPMDTNYPLTQRQTFQGGDNYYNPLTGGAVWGDIKQRYEELGGSNHAIGIPITN
ELPSGTEYFYNNFSNGTISWRNDRQTRFMYLATQRVWDALGRETGRLGFPEADETPEVSG
LFHVA

>RXN03052 TRANSLATE of: rxn03052.seq check: 566 from: 1 to: 756
MPFSHDKSELGGETPYGLVHVNPMAEVRPVKAQTNEPQALQVADIQPFHAVIAASKQLTL
IDVVDVCLGTVLRAWEALSLRWVDVVLDEEHPRIFIRGTIVYNKEKGNHRQDKTKTTSSR
RVIQLPEIASDVLRKRHALYAEHLEMVFPSARGTYIYESNFNKLLRKHRKGTAYDWVTVH
SIRKTLASIVSENLDSKAASDVLGHADSRLTERVYIAKTDKDVPIGDVVNQALKEARKVS
KKSPNKEAKEEE

>RXN03054 TRANSLATE of: rxn03054.seq check: 8742 from: 1 to: 1581
MKLFSKAAGVIAAALLVAGGIAPVAQGQASQVVTPEDQDAYVQQFHHEGNTPPVVDGVGG
YTEQEIAEIHEAIRQAQESGAPNEELIPGEMWSDKVELPVTIDKAAADEAEIAIAQQQSQ
PQTRGLAAAAACQTFWPSPHQVCGAILERYIQQGAQFGWMLFPSEGQTLNPDGQGYRQRF
MNGFVYWHPTTGAHAVNNYSAQVWERNGWESGWMGYPTGGEVPVNGSNPIDGELSGWVQT
FQGGRVYRSPVLDGFQVASINGLILDKWLELGGPDSDLGFPIADEAVTADGVGRFSVFQN
GVVYWHPQHGAHPILGNIYSIWREEGAESGEFGYPIGDPEKYTENMANQVFEKGELAANL
YPNPLEAFIEFLPFANLEEAIEYFENGLSNSRVEANSLNAKKDSIQCQSQSANIHVRTKS
DGVGIRVPKIGFKARMDCDLPGTVSDVVGYGWIYYDYWGRWAQAAYAQQFFGNRNSVVQT
NLEAGCSGEKNTLFWGTSYFQVTYEGQPYFGQSATNYAYLPCTIDRS

>RXN03069 TRANSLATE of: rxn03069.seq check: 6008 from: 1 to: 1083
MHEGRRYSAPYTFGTKGEAQEFLASERTAIINGTWMDFEMRERFEQAQREAEERMMETFF
SYASRWIETRTNAQGKKLSQGVKDDYFRYIKSDRLSYWADYALCEITVADVREWYSDTIQ
DGKLTSMARSYSMMKSVMETAVEDGIIPMNPCKVRGGGNTKTGKKVDVPTDAELEAIIGA
LPSKYFCLAIVAAAGALRFGEIVALRTTDVDVYFDRSGFVDCVRIRISRSIRHTRYHGRV
EGPPKTEAGVRSLYIYGKDAAEIAKHVDTIDVGLRLWSSMRDPDEPMPYHTFKHNWDRAR
ESVHSKATVHSMRHYSGTKYAQVGATLKEVMARLGHSTPSAALRYQHSGERDEELAKRMA
R

>RXN03070 TRANSLATE of: rxn03070.seq check: 3372 from: 1 to: 828
VPALPSSIIDPLWRQFSALIPPVIITHPLGCHRARIADRIIVDKLIAVLVLGVSYIKISD
STCSATTIRTRRDEWITAGIFKNLEQICLESYDRFIGLDLENLNVDGCIVKAPCGGEVAG
RFPVDREKGTKRSLMVDGHGIPIGCVVAGANRHDLPLLAATLDTLGRFGGSLPDQITVHL
DAGYDSKKTRRLLSEFGYSWVISIKGEPLQAGTRWVVERTNSWHNRGFKKLSICTERCTR
VVEAFIALANAVIILRRLIKQAWTSYRWDTRPGHRP

>RXN03078 TRANSLATE of: rxn03078.seq check: 5588 from: 1 to: 480
MTTQDKDLTAQTASRVLSGIQPTADSYHLGNYLGAVKQWIDLQDSYDAFYFIPDLHAITV
DQEPEELRNRTISGAAQLLALGIDPERSTLFVQSHVPAHAELSWVLTCLTGFGEASRMTQ
FKDKSSKRGADRTSAGLFTYPMLMAADILLYRPHLVPVGE

>RXN03102 TRANSLATE of: rxn03102.seq check: 7509 from: 1 to: 492
VVELLKSRGETLAFCESLTAGLASATIAEIPGASVVLKGGLVTYATELKVALAGVPQELI
DAHGVVSPQCARAMATGAAHRCQADWAVSLTGVAGPSKQDGHPVGEVWIGVAGPAHFGAS
GTIDAYRAFESEQQVILAELGRHHIRESAVQQSFRLLIDHIESQ

>RXN03118 TRANSLATE of: rxn03118.seq check: 5261 from: 1 to: 810
MKPTVNVVFNAHHPKDTQPLDKFFDKELKDTHHLDITVGYISEKSLQYLLLIAGTYPDLT
ITLTCGMHAREGMTAAQLHHARVLHDYLSDHDRGGVFVIPRLRYHGKIYLFHKNQHTDPI
AYIGSANLSAIVPGYTSTFEPGVILDPAPEDLVLHLNRDVVPLCVPIDTAHVPIIKDQES
PMKHVAEATAVSTSDVVAIMSSPFTYSFDLKLKATASSNLNAHNSGGGARKQKNGSFLAR
NWYEGEIIVGVETTRLPGYPQNKSEFTAGH

>RXN03121 TRANSLATE of: rxn03121.seq check: 5077 from: 1 to: 642
MHHEQPEGCEVGIRRTIPEESRTAFLDMINQGMSGLAASTAVGVSEFTGRKWAKAAGVKL
TRGPRGGNAFDTAEKLEIAASMLEKGCLPREIGEYVGMTRANISLWRKQGPDKLRQRAAT
LRTGKRAAEFIHAPVMGPYYGPRTLHQVLREDYTTLFDELSALGLPAQVCGALLHLAPPP
SLRFSYMSCVVPLFADEIKIVGQGTRLSLEEKMM

>RXN03130 TRANSLATE of: rxn03130.seq check: 2332 from: 1 to: 1308
MKSTGNIIADTICRTAELGLTITGASDAGDYTLIEADALDYTSTCPECSQPGVFRHHTHR

MLIDLPIVGFPTKLFIRLPRY RCTNPTCKQKYFQAELSCADHGKKVTHRVTRWILQRLAI
DRMSVHATAKALGLGWDLTCQLALDMCRELVYNDPHHLDGVYVIGVDEHKWSHNRAKHGD
GFVTVIVDMTGHRYDSRCPARLLDVVPGRSADALRSWLGSRGEQFRNQIRIVSMDGFQGY
ATASKELIPSARRVMDPFHVVRLAGDKLTACRQRLQREKYQRRGLSQDPLYKNRKTLLTT
HKWLSPRQQESLEQLWAYDKDYGALKLAWLAYQAIIDCYQMGNKREAKKKMRTIIDQLRV
LKGPNKELAQLGRSLFKRLGDVLAYFDVGVSNGPVEAINGRLEHLRGIALGFRNLNHYIL
RCLIHSGQLVHKINAL

>RXN03161 TRANSLATE of: rxn03161.seq check: 570 from: 1 to: 384
MGIFSGRQFPREIILWAVRWYCRYGVSYRDLEEMMTERGVPVDHTTIYRWVQKYAPELDK
KTRWYRQVPDWQARSWRVDETYIRVGGKWCYLYRAITAGSQTLDFYLSPKRNVAAAKRFL
AKTLRSNN

>RXN03165 TRANSLATE of: rxn03165.seq check: 3775 from: 1 to: 321
MGNLPQALRHSFTWDQGVQMAEHARLSVVTKCPVFFCDPHSPWQRGSNENTNGLVRDFFP
KGTNFAKVSDEEVQRAQDMLNYRPRKMHGFKSATQVYEIIVVGASTD

>RXN03168 TRANSLATE of: rxn03168.seq check: 4805 from: 1 to: 1083
MSTRTTPQDRYTDEYGIERVNKDEPGLVDKLRDKHDWFDHLMRMNERFGAKGGNQLSAGI
TYFSVLSIFPIAMLVFGIAGVILAGNPEVLTDIQNRINDALEGEIGNTVNGIIDSAIAQR
GAVLGIGGVTALWSGLGWMANLRFGVSRMWAIDPTEGNFIQKKLTDLVALIVLLLAMGVA
FGITALGASGLTKNLLDFVGLGEIPGISYITWVVAALVGVLANFLVFMWLIFSLPRTKVP
MKPGLQAALLGAIGFEVVKQVGSLLASNALSNPAGAAFGPIIGIMVVLYLIWRILMYCSA
WAATSEEALRLATVPAPEPAIIRVRHEIDPGEEVSQSARKVGIGVAVGAATAGAFALLRK
K

>RXN03169 TRANSLATE of: rxn03169.seq check: 5370 from: 1 to: 438
DLQNPTAKMSKSGDNPKGIINLLDDPKVSTKRIKSAVTDNDGVIAYDPENKPGVSNLLVI
QSALTGTSIDSLVDGYQGAGYGALKGDTADALEAFTTPLKAKYDEYMNDRGELERVLAIG
AERATEVANETLADVYDKIGFLASRR

>RXS00061 TRANSLATE of: RXS00061.seq check: 8093 from: 1 to: 2667
VTEKTDQTLMLIDGHSMAFRAFFALPAENFSTSGGQATNAVYGFLSMLSTLLKDEQPTHVAVAFDVGRK
TFRTDMFPAYKAQREATPPEFKGQVEILKEVLSTLGITTIEKIDFEADDVIATLSVAAKPLGFKTLIVT
GDRDSFQLVNDTTTVLYPMKGVSVLHRFTPEAVEEKYGLTPRQYPEFAALRGDPSDNLPNIPGVGEKTA
TKWIAQYETLDNLLDHADEIKGKVGASLRERIEQVRMNRKLTEMVKDLELPLGPDDFEMKPVQVAEVAA
KFDDLEFGTNLRERVLAVVKAEGSAAPVEEVEAEQVVVDTQSLAQWLPARAGQALALALAGVAKPAAGD
TYALAIADTKRHAVLVDVADISAEDEKALATWLASEDPKMLHGAKAAYHMLAGRGFELHGVVHDTAIAA
YLLRPGQRTYELADVYQRHLQRQLSTNDNGGQLTLLDAADDQSLVDDVIAILELSEELTKQLQEIQAFE
LYHDLEIPLSGILARMEAIGIAVDVATLEEQLKTFIGQVAQEEEAARELAEDPTLNLSSPKQLQVVLFE
TFGMPKTKKTKTGYSTAAAEIEALAIKNPHPFLDHLLAHRQYQKMKTTLEGLIREVAPDGRIHTTFNQT
VASTGRLSSTDPNLQNIPVRTEAGRKIRSGFVVGEGYETLLTADYSQIEMRVMAHLSQDPGLIEAYREG
EDLHNYVGSKVFNVPIDGVTPELRRQVKAMSYGLVYGLSAFGLSQQLSIPAGEAKQIMESYFERFGGVQ
RYLREIVEEARKAGYTETLFGRRRYLPELTSDNRVARENAERAALNAPIQGTAADIIKVAMIRVDRSLK
EAAVKSRVLLQVHDELVVEVAAGELEQVREILEREMDNAIKLSVPLEVSAGDGVNWDAAAH

>RXS00076 TRANSLATE of: RXS00076.seq check: 5232 from: 1 to: 1371
MTTPLRVAVIGAGPAGIYASDLLIRNEEREVFVDLFEQMPAPFGLIRYGVAPDHPRIKGIVKSLHNVLD
KPRLRLLGNIEIGKDITVEELRDYYDAVVFSTGAVADRDLNIPGIEAEGSFGAGEFVGFYDGNPRFERS
WDLSAQSVAVIGVGNVGLDVARILAKTGDELKVTEISDNVYDSLKENKATEVHVFGRRGPAQVKFTPQE
LKELDHSPTINVVVDPEDIDYDGASEEARRASKSQDLVCQILEQYAIREPKDAPHTLQIHLFENPVEVL
QKDGKVVGLRTERTSLDGNGGVNGTGEFKDWPVQAVYRAVGYKSDPIDGVPFDENKHVIPNDGGHVLTA
PGAEPVPGLYATGWIKRGPIGLIGNTKSDAKETTDILIKDAVAGVLEAPKHQGEEAIIELLDSRNIPFT
TWEGWYKLDAAERALGEAEGRERKKIVDWEEMVRQAREAPAIV

>RXS00170 TRANSLATE of: RXS00170.seq check: 511 from: 1 to: 1854
MLLAIGVASPVAQAQVEDQFELVKEISDEQFADDGVDYVPNRNAPTVKEQLEDFESAHPEVVIEYHEHV
NDSKDNVEELPLPKRDIVAGEMRSDVIELPEGVSKDEADQVEVAEARLNEGARLMAATGCEAMWPTGFS
VCGRILDAYRQVGGQLSWLGPPKSNELTNPDGVGKRSEFVGGAIYWHPDTGAYAVTLDGLRQWGTLNWE
SGPLGYPTSGPMDTNYPLTQRQTFQGGDNYYNPLTGGAVWGDIKQRYEELGGSNHAIGIPITNELPSGT

EYFYNNFFNGTISWRNDRQTRFMYLATQRVWDALGRETGRLGFPEADETPEVSGLFHVVNFAERGVIAW
NGILGARELYGDVYSLWLQYQNTDTPLGWPIPSLTSLNESLEQEFTRGVVLGSGDALTWIPDDEERSLE
DFLPIGSSGSSSSSQEMTLFSQRAQYVVDCKNLPDLDEQRKTENNIEKNGGPIKKEYSSRGFPTEFRFVV
RKGHYDRYRNEGWGYLKNYCKHNFANHAMAEAVVDKAVIDYGSSPGTSYYKFEKTVYFLDCRTYTFNKN
SGCKEMHAPQWVTIIYNPHTFTGANSNRPKGVISAWCNSTPPGGIEHEPEISQCPDHVNLYNKLRI

>RXS00212 TRANSLATE of: RXS00212.seq check: 8164 from: 1 to: 1560
MNILCLLCWKFAVRCSSLWRISQEVNAQRIADGGKPFANPRNAAAGSLRQKNIEDVKKRRLRMISHGIG
FTEGFSPASQHDAYLALAAWGLPTSPYTEAVTDPEDVVKKVSYWADHRHDALHEMDGLVIKVDDIASQR
ALGSTSRAPRWAIAYKYPPEEVTTKLLDIQVGVGRTGRVTPFAVMEPVLVAGSTVSMATLHNQSEVKRK
GVLIGDTVVIRKAGEVIPEVLGPVVELRDGTEREYIFPTLCPECGTRLAPAKADDVDWRCPNMQSCPGQ
LSTRLTYLAGRGAFDIEALGEKGAEDLIRTGILLDESGLFDLTEDDLLSSNVYTTNAGKVNASGKKLLD
NLQKSKQTDLWRVLVALSIRHVGPTAARALAGRYHSIQALIDAPLEELSETDGVGTIIAQSFKDWFEVD
WHKAIVDKWAAAGVTMEEEVGEVAEQTLEGLTIVVTGGLEGFTRDSVKEAIISRGGKASGSVSKKTDYV
VIGENAGSKATKAEELGLRILDEAGFVRLLNTGSADE

>RXS00213 TRANSLATE of: RXS00213.seq check: 5673 from: 1 to: 573
VTEDNAQLRRTWNDLAEKVRYHRDRYYNEQPEIPDADFDALFKQLQQLEEDHPELAVPDSPTMVVGAPV
AEQSSFDNVEHLERMLSLDNVFDEQELRDWLGRTPAKQYLTELKIDGLSIDLVYRNGQLERAATRGDGR
VGEDITANARVIEDIPHQLQGTDEYPVPAVLEIRGEVFITVEDFPGGQRAAHC

>RXS00671 TRANSLATE of: RXS00671.seq check: 9925 from: 1 to: 1014
MLISQRPTITEEFVNNARSRFVIEPLEPGFGYTLGNSLRRTLLSSIPGAAVTSVKIDGVLHEFTTISGV
KEDVSDIILNIKGLVLSSDSDEPVVMQLVKEGPGVVTAGDIQPPAGVEIHNPDLHIATLNETAKIEIEL
IVERGRGYVPATVTATGGEIGRIPVDQIYSPVLKVSYKVEATRVEQRTDFDKLVIDVETKNSITARDAL
ASAGKTLVELFGLARELNIAAEGIEIGPSPQETEYIAAYSMPIEDLDFSVRSYNCLKREDIHTVGELAE
RAESDLLDIRNFGQKSINEVKIKLAGLGLTLKDAPEDFDPSTLEGYDAETGGYIDVEAEDSE

>RXS00724 TRANSLATE of: RXS00724.seq check: 5366 from: 1 to: 1977
VGIGDATEGDLVTIVGQVAFAKQSYTQSGKMLYKVTVLTETERIGISFFGAKHIPRLLPEGTRALFTGK
VKFFRNEPQLSHPEFIVIPDPGSGRRLTATGGMKSLAAYGDVEEVALRLVDREYIPIYAGTATMTTWRI
MAAVQRVLETMPVIKEPLSVVPEGMPSFDEAIRGIHDPGHESPSTFINRLKYNEALSLATVMAIRRADT
KNRKAPPMPRALKGHQHMLIDALNFQLTVGQKQVIREISADIEQRVPMSRLLQGEVGSGKTIVSLIAML
QAIDSGRQCAMLAPTEVLATQHARSLSKTLDDAGLDINVVLLTGSMPTGAKKEALLEIISGDADIVVGT
HALIQDTVEFFDLGLVVVDEQHRFGVEQRDQLRTKGREGLTPHLLVMTATPIPRTIAMTVFGDLAVSTL
RELPGGRRPIQTSVIPDHKPGWVKRGWERIGEEVLAGRQAYVVCPRIEGEGGVLEIHAYLSEQVYPGLN
VGMLHGRMDTDLKDSVMQEFAQGEIDILVATTVIEVGIDVANATVMLIREAERFGVSQIHQLRGRVGRG
QHDSLCLLHTTFDEDSPQGQRLAAISTTTDGFQLSELDLQVRQEGDVLGTRQSGSDTKLRHLSFISDQK
IIERALIDATELVAASRSRALELVSDIAMINQEYLEKS

>RXS00823 TRANSLATE of: RXS00823.seq check: 2648 from: 1 to: 780
MGSITPQKRPRVGSHIANKGQETDIGRKRRARRINRTLTVAYPDAHCELDFTNPLELTVATILSAQCTD
VRVNQVTPALFKRYPTATDYANADRTELEEFIRPTGFYRNKATSLIGLGEALISLHDGQVPGTLEQLVE
LPGVGRKTANVVLGNAFGVPGITVDTHFGRLVRRLKLTDEEDPVKVEKVMNELIEKPEWTMFSHRLIFH
GRRICHSRRAACGACMLAADCPSFGLEGPSDPFEAQKLIKSDDREHLLKMAGM

>RXS00898 TRANSLATE of: RXS00898.seq check: 9031 from: 1 to: 789
MRIVNWNVNSARTRVDRMVDFLLRHDVDVLAVQETKCKDEQFPTERFTEIGYEVAHFGLNQWNGVAIIS
RVGIENVETHFPAQPGFNKDITKEQSIEARAIGARCGGVQVWSLYVPNGREIADPHYDYKLRWLFSLRN
YVIDTLEYRPEEKLVLLGDFNIAPTDIDVWDIAAFEGKTHVTEPERAAFDGLIEAGLKETTPGPGTYTY
WDYKGARFLKGEGMRIDFQLASPALAATAGETFVDVEERSGTGASDHAPVIVDYKV
RXS00898 - 5'-Region

>RXS01066 TRANSLATE of: RXS01066.seq check: 7389 from: 1 to: 726
MRRDSFRDRALVVKTYDFGEADRIIVLLTRDHGIVRGVAKGVRRSKSRFGSRLQLFVELDVQLYPGRKL
STISGADTVGYYASGIIEDFTRYSCASAILEIATHIAGLENDPHLFEETTRALKNIQDSPEPILNLDEF
MLRAMNHAGWAPSLFDCAACGRPGPHNAFHPGVGGAVCLYCRPPGSAEVPPEALHMMWLVANGQAARIP
REHPEQQTTIHQLTTAHLQWHIERKLPTLAVLDQA

>RXS01277 TRANSLATE of: RXS01277.seq check: 992 from: 1 to: 2004

MTDYTFLEDIDTPEALAWAEKWSGESVEKLKSPAKDALEARLLAALDTDDRIAYVSRRGEKLYNFWRDA
QHPRGVWRTTTLESYESDQPEWDVLIDVDALAEDEGENWVWKGAVVRSPEFDRALVKFSRGGADATVIR
EFDLATAAFVDDSPFELKEAKSDVTWVDLDTLLVGTDTGEGSLTDSGYPARVLTWKRGTPLEQAELFFE
GSRQDVATHAWRDSTPGFERTFVSRSLDFYNSETSLETEGGLVKLDVPTDCDVIVKKQWIFVSPRTDFA
GIPAGGLGVLLLKEFLEGGRDFQPVFTPTESTSLQGLATTKNFLVLTLLNNVSTEIVTVPLNDPTTEHE
HIDLPEHVTAHVVATSPLDGDEIWVQAASFTEAPTLLRAELPGALEAVKKAPLQFENAGQETRQHWATS
ADGTKIPYFITGAFEEEPQNTLVHAYGGFEVSLTPSHSPTRGIAWLEKGYYFVEANLRGGGEFGPEWHS
QATKLNRMKVWEDHRAVLADLVERGYATPEQIAIRGGSNGGLLTSGALTQYPEAFGAAVVQVPLADMLR
YHTWSAGASWMAEYGNPDDPEERAVIEQYSPVQAVVGVEKRIYPPALVTTSTRDDRVHPAHARLFAQAL
LDAGQAVDYYENTEGGHAGAADNKQTAFVESLIYTWIEKTLDQQGSI

>RXS01438 TRANSLATE of: RXS01438.seq check: 6554 from: 1 to: 1365
MSRPLRVAVVGAGPAGIYASDLLMKSDTDVQIDLFERMPAPFGLIRYGVAPDHPRIKGIVKSLHNVMDK
EQLRFLGNIEVGKDITVEELREFYDAIVFSTGATGDQDLRVPGSDLEGSWGAGEFVGFYDGNPNFERNW
DLSAEKVAVVGVGNVALDVARILAKTGDELLVTEIPDNVYESLAKNQAKEVHVFGRRGPAQAKFTPLEL
KELDHSDTIEVIVNPEDIDYDAASEQARRDSKSQDLVCQTLESYAMRDPKGAPHKLFIHFFESPVEILG
EDGKVVGLKTERTQLDGNGGVTGTGEFKTWDMQSVYRAVGYRSDAIEGVPFDDERAVVPNDGGHIIDPE
VGSPITGLYATGWIKRGPIGLIGNTKSDAKETTEMLLADHAAGSLPAPAKPELESIIEFLDERKVAFTT
WDGWHLLDAAERALGEPEGRERKKIVEWNDMVRHARPEYDI

>RXS02145 TRANSLATE of: RXS02145.seq check: 3306 from: 1 to: 1617
MSLATVGNNLDSRYTMASGIRRQINKVFPTHWSFMLGEIALYSFIVLLLTGVYLTLFFDPSITKVIYDG
GYLPLNGVEMSRAYATALDISFEVRGGLFIRQMHHWAALLFVVSMLVHMLRIFFTGAFRRPREANWIIG
VVLIILGMAEGFMGYSLPDDLLSGVGLRIMSAIIVGLPIIGTWMHWLIFGGDFPSDLMLDRFYIAHVLI
IPAILLGLIAAHLALVWYQKHTQFPGAGRTENNVIGIRIMPLFAVKAVAFGLIVFGFLALLAGVTTINA
IWNLGPYNPSQVSAGSQPDVYMLWTDGAARVMPAWELYLGNYTIPAVFWVAVMLGILVVLLVTYPFIER
KFTGDDAHHNLLQRPRDVPVRTSLGVMALVFYILLTVSGGNDVYAMQFHVSLNAMTWIGRIGLIVGPAI
AYFITYRLCIGLQRSDREVLEHGIETGIIKQMPNGAFIEVHQPLGPVDDHGHPIPLPYAGAAVPKQMNQ
LGYAEVETRGGFFGPDPEDIRAKAKEIEHANHIEEANTLRALNEANIERDKNEGKN

>RXS02308 TRANSLATE of: RXS02308.seq check: 247 from: 1 to: 429
MSETQSNSVSAVMPAQLPPGPAERTVYSYGVRAGDQVHILRMEAFDSDANIVGERDIEAHAEQVFKNLQ
AVIHEAGGTINNIVSTTTYLADVTDAPVVNAARSRYFTGEVLPTHTVIGVAALARPQFLVEISAVAYLG
DLSKD

>RXS02476 TRANSLATE of: RXS02476.seq check: from: 1 to: 879
MSFTAFQTALLVWFRANARDLAWRDPNTSAWGILLSEVMSQQTPVARVEPIWREWMEKWPTPEDFANAS
TDEILRSWGKLGYPRRALRLKECAEVIVEKHAGEVPDTVEALLALPGIGDYTARAVAAFHFGQRVPVVD
TNVRRVYQRAVAGRYLAGPAKKQELIDVSLLLPNTHAPEFSAAIMELGALICTATSPKCDTCPLLDQCQ
WQKLGCPSPSEEELASAKKRVQKFVGTDRQVRGLIMDVLRNATAPVPLSAIDVVWPDDAQRSRALFSLI
EDGLAEQNEAGYFHLPR

>RXS02641 TRANSLATE of: RXS02641.seq check: 9341 from: 1 to: 2076
MLAIILTAVLGASGLAAAGTQYLNTQGEGIGPVAVQNDSESFNSGTNVVVEDAAVTAQGEGGGARTVKE
FQRDQQFSSFALTWTGKKDITAFVRAEQEDGTWSQWYDLEPMVNEDQGTNGTELIWHGPTNKIQVSTLN
VDLFGADAAAADENGQDIPAVDAAEEAAPAAEPAPAEAPVEEAPAPVAEPAPAAEPIAEPVADYSANDGL
APLPSNYGDIQPVADVDDGLNAVFIDGNADAGVGIANVADTDGMPKVISRAGWGADESLRCSNPTIDDG
VSAITIHHTAGSNNYTEAQAAAQVRSAYSYHAKNLGWCDIGYQSLVDKYGNIYEGRAGGMTNAVQGAHA
GGFNQNTWAISMIGDYSYNAPPQETINAVGELAGWRAKVAGFDPTGTDTHYSEGTSYAKYSYGTRVSLP
NILAHRNVGLTACPGDAGYAQMENIRQIVKAKYTSLQNGNTGGTTTTPATTPKETSTSNAPSTTTAQLV
TPAEPQQYSESDALAALLTGGSSGGTDLLNGANSEQLLTGLGSIAAVLIAASLADGGLNGLISNVGSNN
GVPVLGDIKITDVIPIVDTAINLTGDNKYSRGWNDLNNTLGPVLGAATGGETTVKYTSDQNSEVTFVPF
ENGIMVSSPEAGTHGLWGAIGDAWAQQGADLGPLGLPTSNEYTVGEQLRVDFQNGYITYDSATGQASIQ
LN

>RXS02650 TRANSLATE of: RXS02650.seq check: 3610 from: 1 to: 579
MVNVTSKDAGANVTPMSKKEKRTTVKQVVALMAAIVVVIASLDQIVKQIMLSWLEPGVPVPIIGDWFRF
YLLFNPGAAFSMGGENSTWIFTTIQLSFVIGIAIYAPRIKHKWIAAGLALVAGGALGNVLDRLFRDPSF
FFGHVVDYISVGNFAVFNIADASISCGVVVFLIGMFLEDRENAQHAKATDEKDEA

>RXS02760 TRANSLATE of: RXS02760.seq check: 4279 from: 1 to: 954

MSDENINEFEQDEDLNFGASFSDEFADDDFDAEADVEADAAAEASALEAEQDLEEETLDAPEEAAEEAP
AAAESEAPVEEDEEADSLAQAAAALGDTDEQDADAEYKARLRKFTRELKKQPGVWYIIQCYSGYENKVK
ANLDMRAQTLEVEDDIFEVVVPIEQVTEIRDGKRKLVKRKLLPGYVLVRMDMNDRVWSVVRDTPGVTSF
VGNEGNATPVKHRDVAKFLMPQEQAVVTGEAAAAAAEGEQVVAMPTDTKKPQVAVDFTVGEAVTILTGA
FASVSATISSIDPELQKLEVLVSIFGRETPVDLSFDQVEKVS

>RXS02830 TRANSLATE of: RXS02830.seq check: 565 from: 1 to: 648
RRLEDSLGVSLFERAGRGLALTGAGDQLLSQARRLIALNDEVYARLNAGAYEGEVTLGVPQDVIYPVIP
RVLQQFARDFPRVQIHLISNFTLMLKEQFRRGEIDVMLTTEDELGEGGETLAQRELIWVGAPGGSAWTR
RPLPLAFERACIFRSFVQRRLDANSIDWQMVVSSESTRTIEATVSADLAVHTYIEGAEPAHLERIATTA
PCRNYVFQH

>RXS02990 TRANSLATE of: RXS02990.seq check: 3521 from: 1 to: 597
MDIQAEKIEKLRKALDNFERAHARGESDFFDHEKEEKKANVRRRALLLLNQRARSVNELSTRLKALEFE
EDIINEVIGDLTRSKLLDDEVFATEWVRQRAARRGKSSRALDRELQEKGVDKQTRAAALEQIDQADERD
TARAVAVKKARSETKIPQDRADYDKALRRVVGALARRGFPAGMSMDLAREALDARIEDLKN
RXS02990 - 5'-Region
GAAGACTAAGCACCAGTTTTAACAAAGCAGGGACAATCCACACACTTAAACCATGATGTGGCTTGTTCC
TGCTTTTTCGTCAACGAAGGGCAACAACGCG

>RXS03098 TRANSLATE of: RXS03098.seq check: 3946 from: 1 to: 624
MPTTDVFNRVRLALEPLADPARATGMASYMRDQFSFLGIPSTPRKEACKPVLSALKELDTDFVSDCFGA
AEREYQYVACDHINRVGITDLGFAKALVQTKSWWDTVDSLAKPIGAKHDDDLMKTWALDEDFWVRRIAI
IHQLGRKKNTDAALLAWIIEQNLGSSEFFINKAIGWALRDFARHDPSWVRAFVDATDLSPLSRREALKN
I

>RXS03175 TRANSLATE of: RXS03175.seq check: 2273 from: 1 to: 783
VRASEKDTATALQPALDNGWHYIGAPAAAKGRAGVGILSRHELEDVNIGFGSFLDSGRYIEATIKDTTL
DVPVTVASLYLPSGSAGTDKQDEKYRFLDEFEGFLDQRAKERSHMVIGGDWNICHRREDLKNWKTNQKK
SGFLPDERAFMDSVFGTFPDEATQVAGAGDFFGAVDYEGTRRREATTDPAWFDVARRLQPEGDGPYTWW
TYRGKAFDTGAGWRIDYQAATAAMLERAERSWVDKAAAYDLRWSDHSPLNVIYS

>RXS03207 TRANSLATE of: RXS03207.seq check: 2273 from: 1 to: 783
MTAPSTQDLATTEREVDPGSRRGQTNDNPSQDLVRVYLNGIGKTALLTAEDEVELAQTIEVGLYAEHLL
KNSEEPLTRAMKRDLKVLAKDGKKARSHLLEANLRLVVSLAKRYTGRGMPLLDLIQEGNLGLIRAMEKF
DYSKGFKFSTYATWWIRQAITRGMADQSRTIRLPVHLVEQVNKLSRIKRELYQHLGREATNEELAEESG
IEESKIEMLLRQSRDPVSLDMPVGADEEAPLGDFIEDSEATDAESAVVASMRHSDIRAVLNTLEPREQD
VIRLRYGLDDGVPRTLDQIGRRFGLSRERVRQIEREVMSKLRDGERASRLREYAQ